

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 15:55:46 ; Search time 2581.68 Seconds
(without alignments)
3161.255 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

Sequence: 1 ATGCCGCGGACTGCTCCT.....CCCGGTCACCGTCCTAGGT 390

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.pro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg_hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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ALIGNMENTS

RESULT 1

HS285043

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

HS285043 435 bp DNA linear PRI 06-FEB-1997
H.sapiens Ig lambda light chain variable region gene
(24-171TIIH34) rearranged; Ig-Light-Lambda; VLambda.

285043.1 GI:1834754

antigen receptor; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)

Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

XXThe Creation of Diversity in the Human Immunoglobulin V Lambda

Reertoire

J. Mol. Biol. In press

2 (bases 1 to 435)

Ignatovich,O.

Direct Submission

Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein

Engineering, Hills Road, Cambridge CB2 2QH, UK

Engineering, Hills Road, Cambridge CB2 2QH, UK


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QY 361 GGAAGAGGACCGGTTGACCGTCTTAGGT 390
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Db 361 GCGGAGGACCAAGCTGACCGTCTTAGGT 390

RESULT 5
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DEFINITION H.sapiens Ig lambda light chain variable region gene (25-28SWIID60)
rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285358
VERSION 285358.1 GI:1835069
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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(24-09ITIIIC195) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285035
VERSION 285035.1 GI:1834746
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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Best Local Similarity 91.0%; Pred. No. 1.4e-82;
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DEFINITION H.sapiens Ig lambda light chain variable region gene (25-07OIV158)
rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285297
VERSION 285297.1 GI:1835008
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Matches 355; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 ATGGCGCTGACTCTGCTCTGCTCACCCTCCTCACTCAGGGCACAGGATCTGGGCTCAG 60
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rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285355
VERSION 285355.1 GI:1835066
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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Matches 355; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 ATGGCGCTGACTCTGCTCTGCTCACCCTCCTCACTCAGGGCACAGGATCTGGGCTCAG 60
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RESULT 9
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LOCUS H.sapiens Ig lambda light chain variable region gene
DEFINITION (24-12TIIIE213) rearranged; Ig-Lambda; VLambda.
ACCESSION Z85038
VERSION 1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Matches 353; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGGCTTGACTCTGCTCTCTCACCCTCCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
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LOCUS H.sapiens Ig lambda light chain variable region gene
DEFINITION (25-33SWIIE224) rearranged; Ig-Lambda; VLambda.
ACCESSION Z85362
VERSION 1
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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BASE COUNT 76 a 149 c 106 g 104 t
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Query Match 84.8%; Score 330.8; DB 9; Length 435;
Best Local Similarity 90.5%; Pred. No. 1.1e-81;
Matches 353; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGGCTTGACTCTGCTCTCTCACCCTCCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
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JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
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BASE COUNT			
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Matches 352; Conservative			
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Qy	241	GATCGCTTCTTGCTGCCAAGCTCTGGACACACGGCCCTCCCTGACCATCTCTGGGCTCCAG	300
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Qy	301	GCTGAGGACGAGCTGATTATTACTGTGTTTCATATACAACAGTAGGACTTTGTTATTTC	360
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Db	361	GCGGAGGACCAAGCTGACCGTCTAGGT	390
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DEFINITION	HSZ85032	435 bp DNA linear	PRI 06-FEB-1997
ACCESSION		H. sapiens Ig lambda light chain variable region gene (24-05ITIIB54)	
VERSION	285032.1	GI:1834743	
KEYWORDS		immunoglobulin superfamily; rearranged; variable region.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 435)	
TITLE		Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.	
JOURNAL		xxxxThe Creation of Diversity in the Human Immunoglobulin V Lambda Repertoire	
REFERENCE		J. Mol. Biol. In press	
AUTHORS		2 (bases 1 to 435)	
TITLE		Ignatovich,O.	
JOURNAL		Direct Submission	
FEATURES		Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, UK	
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VERSION U43772.1 GI:1353829
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 453)
AUTHORS Boucher,G., Broly,H. and Lemieux,R.
TITLE Restricted Use of Cationic Germline VH Gene Segments in Human Rh(D)
Red Cell Antibodies
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 453)
AUTHORS Boucher,G.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1995) Gerard Boucher, Research and Development,
The Canadian Red Cross Society, Transfusion Center of Quebec, 2535
Laurier Boulevard, Ste-Foy, Quebec G1V 4M3, Canada
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 15:51:41 ; Search time 3874.81 Seconds
(without alignments)
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Title: US-09-019-441-1
Perfect score: 390
Sequence: 1 ATGGCTGGACTGCTCCT.....CCCGTTGACCGTCCTAGGT 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum: *
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6: em_estpl: *
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13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	334	85.6	843	10	BF975970 602246174
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5	329.2	84.4	686	10	BF975970 602246174
6	329.2	84.4	716	9	BF975970 602246174
7	329.2	84.4	767	9	BF975970 602246174
8	329.2	84.4	786	10	BF975970 602246174
9	329.2	84.4	889	10	BF975970 602246174
10	329.2	84.4	908	10	BF975970 602246174
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23	325.8	83.5	611	10	BF975970 602246174
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ALIGNMENTS

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BF975970

LOCUS

DEFINITION

BF975970

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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mRNA sequence.
BF975970
BF975970.1 GI:12343185
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1211 row: c column: 19
High quality sequence stop: 759.
Location/Qualifiers
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FEATURES

Source

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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QY 1 ATGGCTGGACTCTGCTCTCTGCTCACCCTCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
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VERSION      BG756493.1 GI:14067146
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SOURCE       human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 843)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
Plate: LICM1705 row: b column: 10
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FEATURES
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Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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VERSION      BI820758.1 GI:15932308
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SOURCE       human.
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 787)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Life Technologies, Inc.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
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KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Human

REFERENCE
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
JOURNAL Insight into hepatocellular carcinogenesis at transcriptome level
TITLE by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
COMMENT proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
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DB 209 CCAGGCAAGGCCGCCAACTCATGATTTATGATGTGCTTAAGCGGCGCTCAGGGTCTCTCT 268
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Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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QY	361	GGAAGAGGACCCGGTTGACCGTCTTAGGT	390
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<p>RESULT 7</p> <p>AV697043 AV697043 767 bp mRNA linear EST 16-JAN-2002</p> <p>LOCUS AV697043 GK Homo sapiens cDNA clone GKCGW01 5', mRNA sequence.</p> <p>DEFINITION AV697043</p> <p>ACCESSION AV697043</p> <p>VERSION AV697043.1 GI:10298906</p> <p>KEYWORDS EST.</p> <p>SOURCE human.</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 767)</p> <p>AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.</p> <p>TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver</p> <p>JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)</p> <p>MEDLINE 21625106</p> <p>COMMENT Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn This clone is available at CHGC in Shanghai. Location/Qualifiers 1. 767 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="GKCGW01" /clone_lib="GKC" /tissue_type="hepatocellular carcinoma" /dev_stage="Adult" /lab_host="SOLR" /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"</p> <p>BASE COUNT 165 a 249 c 198 g 154 t 1 others</p> <p>ORIGIN</p>			
<p>Query Match 84.4% Score 329.2; DB 9; Length 767;</p> <p>Best Local Similarity 90.3%; Pred. No. 7.7e-78;</p> <p>Matches 35; Conservative 0; Mismatches 38; Indels 0; Gaps 0;</p>			
QY	1	ATGGCGCTGGACTTGCCTCGTCCCTGCTCACCCTCTCACTCAGGGCACAGGATCTCGGGCTCAG	60
Db	29	ATGGCGCTGGGCTGCTGCTATTCTCACCCTCTCACTCAGGGCACAGGCTCTCGGGCCAG	88
QY	61	TCTGCCCGGACTAGCCTCCGCTGTGTCTGGGTCTCTTGGACAGTGGTCAACATCTCC	120
Db	89	TCTGCCCTGACTAGCCTGCGCTGCTGGGTCTCTTGGACAGTGCATCACCTTCTCC	148
QY	121	TGCACTGGAACGACGATGAGTTGGTGTATTAACATATGTCCTCGTACCAACACAC	180
Db	149	TGCACTGGAACGACGATGAGTTGGTAGTTAATCACTATGTCCTGGTACCAACAC	208
QY	181	CCAGGCAAGCCGCCAACACTCATGATTTATGATCTCGTACGCGGGCTCAGGGGTCTCT	240
Db	209	CCAGGCAAGCCGCCAACGATCATGATTTATGATCTCAATATCGCCCTCAGGGGTCTCT	268
QY	241	GATCGCTTCTGGCTCCAAGTCTGGCAACACGGCTCCCTCGACATCTCTGGGCTCCAG	300
Db	269	AATCGCTTCTGGCTCCAAGTCTGGCAACACGGCTCCCTCGACATCTCTGGGCTCCAG	328

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QY 181 CCAGCAAGAGCCCAAACTCATGATTATGATGTCGTAAGCGGCGCTCAGGGTCTCT 240
Db 212 CCAGCAAGAGCCCAAACTCATGATTATGAGGTCAATAAGCGGCGCTCAGGGTCTCT 271
QY 241 GATCGCTTCTCTGGCTCAAGTCTGGCAACACAGCGGCTCCCTGACCACTCTGGGCTCCAG 300
Db 272 GATCGCTTCTCTGGCTCAAGTCTGGCAACACAGCGGCTCCCTGACCGTCTCTGGGCTCCAG 331
QY 301 GCTGAGGACGAGGCTGATTATTTACTGTTTCATATACACAGCTAGACATTTGTTATTC 360
Db 332 GCTGAGGATGAGGCTGATTATTTACTGCAGCTCATATGCGAGCAGCAACAATATGTTCTTC 391
QY 361 GGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 390
Db 392 GGAAGTGGGACCAAGGTCACCGTCTCTAGGT 421

RESULT 9
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LOCUS 602713662F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853919 5',
DEFINITION mRNA sequence.
ACCESSION BG756342
VERSION BG756342.1 GI:14066995
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1700 row: 1 column: 16
High quality sequence stop: 810.
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1..889
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4853919"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 215 a 289 c 222 g 163 t
ORIGIN

Query Match 84.4%; Score 329.2; DB 10; Length 889;
Best Local Similarity 90.3%; Pred. No. 8.1e-78;
Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGGCGCTGACTCTGCTCGTCAACCTCTACTGAGGACAGGATCTGGGCTCAG 60
Db 32 ATGGCGCTGGGCTCTGCTCTCAACCTCTCTACTGAGGACAGGATCTGGGCTCAG 91

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QY 61 TCTCCCCGACTCAGCCTCCCTCTGTCTGTCTGGGTCTCTCTGGACAGTGGTACCATCTCC 120
Db 92 TCTCCCTGACTCAGCCTCCCTCCGCGTCTCTCTGGACAGTCAATGTCACCATCTCC 151
QY 121 TGCACCTGGAACCCAGGATGAGCTTGGTGGTTATTAACATATGTCCTCTGTTACCAACACAC 180
Db 152 TGCACCTGGAACCCAGGATGAGCTTGGTGGTTATTAACATATGTCCTCTGTTACCAACACAC 211
QY 181 CCAGGCAAGAGCCCAAACTCATGATTATGATGTCGTAAGCGGCGCTCAGGGTCTCT 240
Db 212 CCAGGCAAGAGCCCAAACTCATGATTATGAGGTCAATAAGCGGCGCTCAGGGTCTCT 271
QY 241 GATCGCTTCTCTGGCTCAAGTCTGGCAACACAGCGGCTCCCTGACCACTCTCTGGGCTCCAG 300
Db 272 GATCGCTTCTCTGGCTCAAGTCTGGCAACACAGCGGCTCCCTGACCGTCTCTCTGGGCTCCAG 331
QY 301 GCTGAGGACGAGGCTGATTATTTACTGTTTCATATACACAGCTAGACATTTGTTATTC 360
Db 332 GCTGAGGATGAGGCTGATTATTTACTGCAGCTCATATGCGAGCAGCAACAATATGTTCTTC 391
QY 361 GGAAGAGGAGCCCGGTTGACCGTCTCTAGGT 390
Db 392 GGAAGTGGGACCAAGGTCACCGTCTCTAGGT 421

RESULT 10
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LOCUS 602710363F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850871 5',
DEFINITION mRNA sequence.
ACCESSION BG756874
VERSION BG756874.1 GI:14067527
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1692 row: m column: 16
High quality sequence stop: 885.
FEATURES
source
1..908
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/db_xref="taxon:9606"
/clone="IMAGE:4850871"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 217 a 292 c 229 g 168 t
ORIGIN

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 16:01:56 ; Search time 488.47 Seconds
(without alignments)
1370.804 Million cell updates/sec

Title: US-09-019-441-1
Perfect score: 390
Sequence: 1 ATGGCTGGACTCTGCTCT...CCCCGGTGGACCGTCTAGGT 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	AAV33307	Anti-human CD23 6G
2	321.2	82.4	891	AA66528	Human immune syste
3	319.6	81.9	902	AAQ35100	Antibody D lambda
4	316.4	81.1	889	AA377073	DNA encoding novel
5	313.6	80.4	763	AA583480	DNA encoding novel
6	310	79.5	448	AA577070	DNA encoding novel
7	307.2	78.8	7528	AA330316	Bicistronic idioxy
8	306.8	78.7	756	AA583477	DNA encoding novel
9	306.8	78.7	866	AA587037	DNA encoding novel

10	305.2	78.3	453	23	AA577071	DNA encoding novel
11	303.6	77.8	637	23	AA577074	DNA encoding novel
12	298.8	76.6	783	23	AA583483	DNA encoding novel
13	298.6	76.6	414	23	AA577069	DNA encoding novel
14	297	76.2	863	23	AA583485	DNA encoding novel
15	295.6	75.8	876	23	AA583478	DNA encoding novel
16	295.2	75.7	548	21	AA68957	Human ovarian carc
17	292.4	75.0	351	22	AA168755	Human autoantibody
18	284.6	73.0	628	14	AAQ36134	MH4H7 MAB light ch
19	284.6	73.0	1044	12	AAQ12840	Variable region of
20	284.4	72.9	351	22	AA168765	Human autoantibody
21	281.2	72.1	747	21	AA67868	Recombinant human
22	280.8	72.0	333	22	AAH42401	Nucleotide sequenc
23	280.8	72.0	333	22	AAH42407	Nucleotide sequenc
24	278.4	71.4	9071	13	AAQ22491	Human U266 lambda
25	278.4	71.4	9071	13	AAQ23370	U266-Lambda gene a
26	275.4	70.6	333	17	AA10327	Human anti-Pseudom
27	275.4	70.6	333	20	AA231655	Coding sequence fo
28	274.8	70.5	351	22	AA168759	Human autoantibody
29	273.8	70.2	333	20	AA231654	Coding sequence fo
30	271.2	69.5	729	22	AAH47763	Anti-hEDRF antibod
31	270.8	69.4	330	22	AA503477	DNA encoding anti-
32	269.2	69.0	330	22	AA503520	DNA encoding anti-
33	269	69.0	342	21	AA62337	DNA encoding a var
34	265.8	68.2	333	15	AAQ55659	Monoclonal antibod
35	263	67.4	777	23	AA577072	DNA encoding novel
36	261.8	67.1	360	24	ABA94221	EBV transformant a
37	258	66.2	336	22	AA503509	DNA encoding anti-
38	258	66.2	529	23	AA579448	DNA encoding novel
39	249.2	63.9	717	22	AA58707	Huntingtin intrabo
40	248.4	63.7	327	22	AA58706	Huntingtin minimal
41	246.8	63.3	747	22	AAH76382	Nucleotide sequenc
42	246.6	63.2	375	20	AAV72228	Human anti-GPIIb/I
43	246.4	63.2	336	22	AAH42391	Nucleotide sequenc
44	244.4	62.7	402	22	AAH35419	Human colon cancer
45	241.8	62.0	482	22	ABA58301	Human foetal liver

ALIGNMENTS

RESULT 1
ID AAV33307 standard; DNA; 390 BP.

AAV33307;

18-NOV-1998 (first entry)

Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.

Anti-human CD23 6G5 monoclonal antibody; light chain variable region;
human CD23; Ig; FcεRII/CD23; gamma-1 constant region;
gamma-3 constant region; allergy; inflammation; autoimmune disease;
allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

Macaca fascicularis

Key Location/Qualifiers

CDS 1..390
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/product= "anti-human CD23 6G5 light chain variable region"

FT sig_peptide /note= "CDS does not contain a stop codon"

FT mat_peptide /tag= b

FT misc_feature /tag= c

FT misc_feature /tag= d

FT misc_feature /note= "encodes CDR 1 region"

FT /*tag= e

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FT misc_feature /note="encodes CDR 2 region"  
FT 328..357 /*tag= f  
FT /note="encodes CDR 3 region"  
XX  
PN WO9837099-A1.  
XX  
XX 27-AUG-1998.  
XX  
XX 17-FEB-1998; 98WO-US02253.  
XX  
XX 05-FEB-1998; 98US-0803085.  
PR 20-FEB-1997; 97US-0803085.  
XX  
XX (IDEC-) IDEC PHARM CORP.  
PA (SEK ) SEIKAGAKU CORP.  
XX  
XX Kloetzer WS, Nakamura T, Reff ME;  
PI  
XX WPI; 1998-467495/40.  
DR P-PSDB; AAW70377.  
XX  
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE  
PT expression to treat or prevent allergic, inflammatory and  
PT auto:immune conditions  
XX  
XX Example 1; Pages 102-104; 146pp: English.  
XX  
XX The present sequence represents a DNA sequence encoding the light  
CC chain variable region of primate monoclonal antibody anti-human CD23 6G5.  
CC The invention provides primates monoclonal antibodies which specifically  
CC bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),  
CC and comprise either a human gamma-1 or human gamma-3 constant region  
CC that binds to human Fc gamma receptors and inhibits IgE expression.  
CC The monoclonal antibodies of the invention are claimed to be useful  
CC for inhibiting induced IgE production for treating or preventing  
CC allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis  
CC conjunctivitis, autoimmune haemolytic anaemia, etc.  
XX  
XX Sequence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;  
SQ  
  
Query Match 100.0%; Score 390; DB 19; Length 390;  
Best Local Similarity 100.0%; Pred. No. 1.6e-109;  
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 atggcttgactctgtctctgtctcctcctcactcaggacaggatcctgggctcag 60  
  
QY 61 TCTGCCCCGACTCAGCTCCCTCTGTCTGTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120  
DB 61 tctgccccgactcagctccctctgtctgtggtctctcctggacagtcggtcaccatctcc 120  
  
QY 121 TGCACTGGAAACGACGATGACGTTGGTGGTTAATACTATGTCCTCGGTACCAACACCAC 180  
DB 121 tgcactggaaacgacgatgactgtggtggttataactatgtctcctggtaaccaaccac 180  
  
QY 181 CCAGGCAAGGCCCCAAACTCATGATTATGATGTCGTAAAGCGGCCTCAGGGGTCTCT 240  
DB 181 ccaggcaaggcccccAAACTCATGATTATGATGTCGTAAAGCGGCCTCAGGGGTCTCT 240  
  
QY 241 GATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 300  
DB 241 gatcgcttctctggctcccaagtctggcaacacggccctccctgaccatctctgggctccag 300  
  
QY 301 GCTGAGGACGAGCTGATTATTACTGTTTTCATATACACAGTAGAGACTTGTGTTATTC 360  
DB 301 gctgaggacgagctgattattactgttttcataacacagtagagacttgtgttatttc 360  
  
QY 361 GGAAGAGGACCGGTTGACCGTCTAGGT 390  
DB 361 ggaagaggacccgggttgaccgtctcctagggt 390
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RESULT 2  
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ID AAC66528 standard; cDNA; 891 BP.  
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XX AAC66528;  
XX  
XX 15-FEB-2001 (first entry)  
XX  
XX Human immune system associated protein HISAP-10 coding sequence.  
DE  
XX Human immune system associated protein; HISAP-10; immune disorder;  
KW infection; autoimmune disease; cancer; ss.  
KW  
XX Homo sapiens.  
OS  
XX US6135941-A.  
PN  
XX 24-OCT-2000.  
PD  
XX 27-MAR-1998; 98US-0049672.  
PF  
XX 27-MAR-1998; 98US-0049672.  
PR  
XX (INCY-) INCYTE PHARM INC.  
PA  
XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
PI Hillman JL, Au-Young J;  
XX  
XX WPI; 2001-030926/04.  
DR P-PSDB; AAB63212.  
XX  
XX New human immune system associated proteins (HISAP) and polynucleotides  
PT encoding the HISAP, useful for diagnosing, treating or preventing  
PT immune or cell proliferative disorders or infections  
XX  
XX Claim 3; Column 87-90; 54pp: English.  
PS  
XX The present invention provides the coding and protein sequences for a  
CC number of human immune system associated proteins (HISAPs). These can be  
CC used in the diagnosis and treatment of various autoimmune disorders,  
CC infections and cell proliferation diseases. The diseases include AIDS,  
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
CC erythematosus, arteriosclerosis, cirrhosis and cancer.  
XX  
XX Sequence 891 BP; 207 A; 287 C; 222 G; 175 T; 0 other;  
SQ  
  
Query Match 82.4%; Score 321.2; DB 22; Length 891;  
Best Local Similarity 89.0%; Pred. No. 2.4e-88;  
Matches 347; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
  
QY 1 ATGGCTTGACTCTGCTCTGCTCCTCCTCAGGACACAGGATCCTGGGCTCAG 60  
DB 34 atggcttgactctgtctctgtctcctcactcactcaggacagggtcctgggcccag 93  
  
QY 61 TCTGCCCCGACTCAGCTCCCTCTGTCTGTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120  
DB 94 tctgccccgactcagctccctctgtctgtggtctcctggacagtcgataccatctcc 153  
  
QY 121 TGCACTGGAAACGACGATGACGTTGGTGGTTAATACTATGTCCTCGGTACCAACACCAC 180  
DB 154 tgcactggaaacgacgatgactgtggtggttataactatgtctcctcggtaaccaactcc 213  
  
QY 181 CCAGGCAAGGCCCCAAACTCATGATTATGATGTCGTAAAGCGGCCTCAGGGGTCTCT 240  
DB 214 ccaggcaaggcccccAAACTCATGATTATGATGTCGTAAAGCGGCCTCAGGGGTCTCT 273  
  
QY 241 GATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAG 300  
DB 241 gatcgcttctctggctcccaagtctggcaacacggccctccctgaccatctctgggctccag 300
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Db 274 aatcggttctctggtccaaagctggaacacagggctccctgaccatctctctgggtccag 333
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 |||||
 Db 334 gctgagacgaggtgattattactgagctcatgtaggaacaacattggtatttc 393
 QY 361 GGAAGAGGACCGGTTGACCGTCCTAGGT 390
 || |||||
 Db 394 ggcggaggaccacagctgaccgtccctaggt 423

RESULT 3

AAQ35100
 ID: AAQ35100 standard; DNA; 902 BP.

XX AC AAQ35100;

XX DT 19-MAY-1993 (first entry)

XX DE Antibody D lambda light chain.

XX KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;

KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;

KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H; ss.

XX OS Synthetic.

XX FH Key

FT CDS

FT Location/Qualifiers

FT 32..739

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FT sig_peptide

FT 32..88

FT /*tag= b

FT misc_RNA

FT 89..154

FT /*tag= c

FT misc_RNA

FT 155..196

FT /*tag= d

FT misc_RNA

FT 197..242

FT /*tag= e

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FT 243..262

FT /*tag= f

FT misc_RNA

FT 263..358

FT /*tag= g

FT misc_RNA

FT 359..388

FT /*tag= h

FT misc_RNA

FT 389..421

FT /*tag= i

FT misc_RNA

FT 422..736

FT /*tag= j

FT TATA_signal

FT 842..847

FT /*tag= k

FT TATA_signal

FT 853..858

FT /*tag= l

XX EP523949-A.

XX DT 20-JAN-1993.

XX 14-JUL-1992; 92EP-0306420.

XX 15-JUL-1991; 91GB-0015284.

XX 01-AUG-1991; 91GB-0016594.

XX 23-MAR-1992; 92GB-0006284.

XX (WELL) WELLCOME FOUND LTD.

PI

XX Crowe JS, Lewis AP;

XX WPI; 1993-019951/03.

DR P-PSDB; AAR31025.

XX Prodn. of recombinant primate antibodies - useful for treating

PT infections caused by hepatitis A, B and C, herpes,

PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,

PT arthritis etc.

XX PS Disclosure; Fig 3; 35pp; English.

XX CC The sequences given in AAQ35099-100 encode the heavy and light chains

CC of Antibody D respectively. Antibody D is a monoclonal antibody which

CC was derived from peripheral blood lymphocytes from a hepatitis A virus

CC (HAV) sero positive patient. Antibody D is closely related in nature

CC to murine antibody B5B3. Total RNA was isolated from antibody D

CC expressing cells and polyadenylated RNA was extracted. These polyA

CC RNA's were used to prepare a cDNA library which was screened for human

CC kappa light (L) chains and two positive clones were detected.

CC Further heavy (H) chain clones were also isolated.

XX Sequence 902 BP; 225 A; 285 C; 218 G; 174 T; 0 other;

QY

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

QY

1

ATGGCGTGGAC

CTGCTCGT

CACCCCTC

CTCCTC

CACCTC

CACCTC

CACCTC

CACCTC

CACCTC

CACCTC

CACCTC

CACCTC

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CACCTC

PN WO200109303-A2.
XX 08-FEB-2001.
XX 31-JUL-2000; 2000WO-US20679.
XX 30-JUL-1999; 99US-0146170.
XX (VICA-) VICAL INC.
XX Hermanson GG;
XX WPI; 2001-123319/13.
XX Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX Example 2; Page 101-106; 149pp; English.
XX The present sequence is that of patient-specific bicistronic
CC chimeric idiotype VRI642 (Plasmid VAXID), which is used to treat
CC B-cell lymphoma patients. The plasmid includes the cytomegalovirus
CC immediate-early promoter, enhancer and 5' untranslated sequences,
CC driving the expression of mouse-human chimeric immunoglobulin
CC light and heavy chain sequences. The human light and heavy chain
CC variable regions are derived from B-cell lymphoma cell line RAMOS.
CC The transcriptional terminator region includes polyA and termination
CC signals from the bovine growth hormone gene. According to the
CC invention, co-administration of VRI642 with a plasmid (see AAF30314)
CC encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a
CC means of treating a patient with B-cell lymphoma.
XX Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;

Query Match 78.8%; Score 307.2; DB 22; Length 7528;
Best Local Similarity 88.3%; Pred. No. 1.1e-83;
Matches 346; Conservative 0; Mismatches 43; Indels 3; Gaps 1;
QY 1 ATGGCTGGACTGCTGCTCCCTGACCTCTCCTCAGTCAGGACAGATCTGGGCTCAG 60
Db 6 atggcctgggctctgctgctccacccctcactcaggagcaggtcctgggcccag 65
QY 61 TCTGCCCGGACTCAGCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 66 tctgccctgactcagctgctcctgctgctgctgctgctgctgctgctgctgctgct 125
QY 121 TGCAGTGAACAGCGATGACGTTGGTGGTTAATATATCTCTCTGCTGCTGCTGCTGCT 180
Db 126 tgcactggaaccagcagtgatgtgtggaggtataaccctgtctcctggtaccacaaac 185
QY 181 CCAGGCAAGCCGCCAAACATCATGATTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 186 ccaggcaagcccccacaaactcagttatgattgattgattgattgattgattgatttct 245
QY 241 GATCGCTTCTCTGCTGCTCCTCAAGTCTGCAACACGCTCCTGCTGCTGCTGCTGCTGCT 300
Db 246 aatcgcttctctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 305
QY 301 GCTGAGACAGCGCTGATTATTAATGTTGTTATATACACAGTAGTAGCA---CTTTGTTA 357
Db 306 gctgacgacgaggtgattattactgcaacctatatacaaacgacagcaattctcaggta 365
QY 358 TTCGGAAGGGACCGGTTGACCGTCTAGG 389
Db 366 ttcggcggaggcccaagctgacctcctagg 397

RESULT 8
AAS83477
ID AAS83477 standard; cDNA; 756 BP.

XX AAS83477;
XX 13-FEB-2002 (first entry)
XX DNA encoding novel human diagnostic protein #19281.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG19290.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX Claim 1; SEQ ID NO 19281; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 756 BP; 161 A; 240 C; 197 G; 158 T; 0 other;

Query Match 78.7%; Score 306.8; DB 23; Length 756;
Best Local Similarity 86.7%; Pred. No. 5.9e-84;
Matches 338; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 1 ATGGCTGGACTGCTGCTCCTGCTCAGCTCCCTCCTCAGTCAGGACAGATCTGGGCTCAG 60
Db 1 atggcctggactctgctattctccaccctcctcactcagggccacaggtcctggggcccag 60
QY 61 TCTGCCCGGACTCAGCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 tctgccctgactcagctgctcctcctgctgctgctgctgctgctgctgctgctgctgct 120
QY 121 TGCAGTGAACAGCGATGACGTTGGTGGTTAATATATGCTCTCTGCTGCTGCTGCTGCT 180

Db 241 gatcgttctctgctccatgtctgccaacacggtccctccctgacaaatctctctgggtccag 300
QY 301 GCTGAGACGAGCTGATTATTAATCTGTTTCATATACACAGTAGCAC---TTTGTGTTA 357
Db 301 gctgacgacgaggtgattattactgctgctgctggttagtcgagcgcctctgaatc 360
QY 358 TTCGGAAGAGGACCGGTGACCGTCCCTAGGT 390
Db 361 ttcggaagtggaccaggtcatcgctcaggt 393

RESULT 15

AAS83478
ID AAS83478 standard: cDNA; 876 BP.

XX AC AAS83478;
XX

XX 13-FEB-2002 (first entry)
XX

XX DE DNA encoding novel human diagnostic protein #19282.
XX

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX OS

XX PN WO200175067-A2.
XX

XX PD 11-OCT-2001.
XX

XX PF 30-MAR-2001; 2001WO-US08631.
XX

XX PR 31-MAR-2000; 2000US-0540217.
XX

XX PR 23-AUG-2000; 2000US-0649167.
XX

XX PA (HYSE-) HYSEQ INC.
XX

XX PI Drmanac RT, Liu C, Tang YT;
XX

XX DR WPI; 2001-639362/73.
XX

XX DR P-PSDB; ABG19291.
XX

XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX

XX PS Claim 1; SEQ ID NO 19282; 103pp; English.
XX

XX CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

XX SQ Sequence 876 BP; 193 A; 294 C; 225 G; 164 T; 0 other;

Query Match 75.8%; Score 295.6; DB 23; Length 876;
Best Local Similarity 86.1%; Pred. No. 1.7e-80;
Matches 341; Conservative 0; Mismatches 49; Indels 6; Gaps 1;

QY 1 ATGGGCTGACACTCTGCTCCCTCGCTCACCCCTCCACACAGGACAGATCCTGGGCTCAG 60
Db 44 atggcctgggctctgctcatcctcaccctccctcaactcagggcacagggctctggggcccg 103
QY 61 TCTGCCCCGACTCAGCCTCCCTCTGTGTGGGTCTCCCTGGAGAGTCGGTACACATCTCC 120
Db 104 tctgccccgaactcagcctccctccggtctctggacagtcagtcacattctcc 163
QY 121 TGCACCTGGAAACAGCAGATGACGTTGGTGTATATACTATCTCTCTGGTACCAACACAC 180
Db 164 tgcagtggaaaccagcagtgacattggttaataataattatctctctgggtaccgacaacac 223
QY 181 CCAGGCAAAAGCCCCCAAACTCATGATTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCT 240
Db 224 ccaggcaaaagcccccaaaactcatgtctatgaggtcactaagcggccctcaggggtccct 283
QY 241 GATCGCTTCTCTGGCTCCCAAGTCTGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 284 aaccgtctctctggctccaagtctggcaacacggtccctccctgacctctctgggtccag 343
QY 301 GCTGAGGACGAGGCTGATTACTTACTTGTGTTCATATACACACAGTAGCAC-----TTTG 354
Db 344 gctgaggtatgaggtgattattactgtctcatatgctcagggcgactacaccccggtcg 403
QY 355 TTATTTCGGAAGAGGACCGGTGACCGTCCCTAGGT 390
Db 404 gtttcggtggaggggaccaggtgacctcctcaggt 439

Search completed: September 23, 2002, 17:58:36
Job time: 7000 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:59:10 ; Search time 662.78 Seconds
(without alignments)
1896.375 Million cell updates/sec

Title: US-09-019-441-1
Perfect score: 390
Sequence: 1 ATGGCCTGACTCTGCTCT.....CCGGTTGACCGTCTAGCT 390

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
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6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	7	US-10-103-686-1
2	327.6	84.0	1640	6	Sequence 1, Appli
3	326.6	83.7	1597	6	Sequence 13206, A
4	324.4	83.2	408	5	US-10-198-846-13206
5	324.4	83.2	421	5	Sequence 13540, A
6	313.2	80.3	1597	6	Sequence 36573, A
7	311.6	79.9	420	5	US-09-918-995-16692
8	305.4	78.3	1636	5	Sequence 13540, A
9	305.4	78.3	1636	5	Sequence 16500, A
10	301.8	77.4	883	7	Sequence 22578, A
11	300.6	77.1	2667	7	Sequence 28418, A
12	295.2	75.7	548	6	Sequence 73, Appl
13	295.2	75.7	1636	5	Sequence 267, Appl
14	295.2	75.7	1636	5	Sequence 76, Appl
15	288	73.8	413	5	Sequence 22578, A
16	285.4	73.2	735	7	Sequence 28418, A
17	285.4	73.2	735	7	Sequence 16199, A
18	285.4	73.2	735	7	Sequence 59, Appl
19	285.4	73.2	735	7	Sequence 63, Appl
20	285.4	73.2	735	7	Sequence 64, Appl
21	285.4	73.2	735	7	Sequence 59, Appl
22	284.6	73.0	331	1	Sequence 63, Appl
23	284.6	73.0	331	1	Sequence 64, Appl
24	284.4	72.9	726	1	Sequence 200, App
25	284.4	72.9	726	1	Sequence 200, Appl

26	281.2	72.1	747	5	US-09-959-373A-1	Sequence 1, Appli
27	281.2	72.1	819	1	PCT-US02-18947-198	Sequence 138, App
28	281.2	72.1	819	7	US-10-172-118-198	Sequence 198, App
29	280.4	71.9	12220	5	US-09-919-002-67	Sequence 67, Appl
30	279.6	71.7	435	5	US-09-918-995-16554	Sequence 16554, A
31	275.8	70.7	735	7	US-10-039-785-54	Sequence 54, Appl
32	275.8	70.7	735	7	US-10-139-785-54	Sequence 54, Appl
33	275.8	70.7	735	7	US-10-139-785-54	Sequence 54, Appl
34	273.2	70.1	530	5	US-10-027-632-18093	Sequence 18093, A
35	269.4	69.1	735	7	US-09-785-276A-56598	Sequence 56598, A
36	269.4	69.1	735	7	US-10-039-785-57	Sequence 57, Appl
37	267.8	68.7	735	7	US-10-139-785-60	Sequence 60, Appl
38	267.8	68.7	735	7	US-10-039-785-60	Sequence 60, Appl
39	261.4	67.0	735	7	US-10-139-785-58	Sequence 58, Appl
40	261.4	67.0	735	7	US-10-039-785-61	Sequence 61, Appl
41	261.4	67.0	735	7	US-10-139-785-58	Sequence 58, Appl
42	261.4	67.0	735	7	US-10-139-785-61	Sequence 61, Appl
43	258.2	66.2	735	7	US-10-039-785-55	Sequence 55, Appl
44	258.2	66.2	735	7	US-10-139-785-55	Sequence 55, Appl
45	237.6	66.1	496	5	US-09-918-995-37811	Sequence 37811, A

ALIGNMENTS

RESULT 1
US-10-103-686-1
; Sequence 1, Application US/10103686
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/103,686
; FILING DATE: 25-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..390
; FEATURE:
; NAME/KEY: mat_peptide

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; LOCATION: 58..390
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

Query Match      100.0%; Score 390; DB 7; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCTGACTCTGCTCGTCAACCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAG 60
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Db 1 ATGGCGCTGACTCTGCTCGTCAACCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAG 60
    |||||||
Qy 61 TCTGCCCGGACTCAGCCCTCCTCTGTGCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||||
Db 61 TCTGCCCGGACTCAGCCCTCCTCTGTGCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||||
Qy 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATTAATATGTCCTGGTACCAACACCAC 180
    |||||||
Db 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATTAATATGTCCTGGTACCAACACCAC 180
    |||||||
Qy 181 CCAGGCAAGCCCAAACTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCT 240
    |||||||
Db 181 CCAGGCAAGCCCAAACTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCT 240
    |||||||
Qy 241 GATCGCTTCTCTGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||||
Db 241 GATCGCTTCTCTGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||||
Qy 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACAAACAGTAGACACTTTGTTATTTC 360
    |||||||
Db 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACAAACAGTAGACACTTTGTTATTTC 360
    |||||||
Qy 361 GGAAGAGGACCGGTTGACCGTCTCTAGGT 390
    |||||||
Db 361 GGAAGAGGACCGGTTGACCGTCTCTAGGT 390
    |||||||

RESULT 2
US-10-198-846-13206/c
; Sequence 13206, Application US/10198846
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13206
; LENGTH: 1640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13206

Query Match      84.0%; Score 327.6; DB 6; Length 1640;
Best Local Similarity 90.0%; Pred. No. 2.3e-80;
Matches 351; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 ATGGCGCTGACTCTGCTCGTCAACCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAG 60
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Db 1569 ATGGCGCTGGGCTCTGCTCTCTCAGCGCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAG 1510
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Qy 61 TCTGCCCGGACTCAGCCCTCCTGTGCTGGGTCTCTGGACAGTCGGTCACCATCTCC 120
    |||||||

; LOCATION: 58..390
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

Query Match      100.0%; Score 390; DB 7; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCTGACTCTGCTCGTCAACCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAG 60
    |||||||
Db 1 ATGGCGCTGACTCTGCTCGTCAACCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAG 60
    |||||||
Qy 61 TCTGCCCGGACTCAGCCCTCCTCTGTGCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||||
Db 61 TCTGCCCGGACTCAGCCCTCCTCTGTGCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||||
Qy 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATTAATATGTCCTGGTACCAACACCAC 180
    |||||||
Db 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATTAATATGTCCTGGTACCAACACCAC 180
    |||||||
Qy 181 CCAGGCAAGCCCAAACTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCT 240
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Db 181 CCAGGCAAGCCCAAACTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCT 240
    |||||||
Qy 241 GATCGCTTCTCTGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
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Db 241 GATCGCTTCTCTGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
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Qy 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACAAACAGTAGACACTTTGTTATTTC 360
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Db 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACAAACAGTAGACACTTTGTTATTTC 360
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Qy 361 GGAAGAGGACCGGTTGACCGTCTCTAGGT 390
    |||||||
Db 361 GGAAGAGGACCGGTTGACCGTCTCTAGGT 390
    |||||||

RESULT 3
US-10-198-846-13540/c
; Sequence 13540, Application US/10198846
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13540
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13540

Query Match      83.7%; Score 326.6; DB 6; Length 1597;
Best Local Similarity 90.0%; Pred. No. 4.3e-80;
Matches 350; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 2 TGGCGCTGGACTCTGCTCGTCAACCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAGT 61
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Db 1529 TGGCGCTGGGCTCTGCTCGTCAACCTCCTCACTCAGGCGCACAGGATCCTGGGCTCAGT 1470
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Qy 62 CTGCCCCGACTCAGCCTCCCTCTGTGCTGGGTCTCTCGGACAGTCGGTCACCATCTCTCT 121
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Db 1469 CTGCCCCGACTCAGCCTCCCTCTGTGCTGGGTCTCTCGGACAGTCGATCACCATCTCT 1410
    |||||||
Qy 122 GCACCTGGAAACGAGGATGACGTTGGTGGTTATTAATATGTCCTCTGGTACCAACACCAC 181
    |||||||
Db 1409 GCATTGGAAACCTCAATGACATGGTAGTTATTAATATGTCCTCTGGTACCAACACCAC 1350
    |||||||
Qy 182 CAGGCAAGCCCCCAAACTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTG 241
    |||||||
Db 1349 CAGGCAAGCCCCCAAACTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTG 1290
    |||||||
Qy 242 ATCGGCTCTCTGGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 301
    |||||||
Db 1289 ATCGGCTCTCTGGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 1230
    |||||||
Qy 302 CTGAGGACGAGGCTGATTTACTGTTGTCATATACAAACAGTAGACACTTTGTTATTTC 361
    |||||||
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Query Match	75.7%	Score 295.2	DB 6	Length 548
Best Local Similarity	87.7%	Pred. No. 1.6e-71		
Matches 343	Conservative	0	Mismatches 46	Indels 2
QY 1	ATGGCCTGGACTGTGCTCTGTGTCACCTCTCTACTCAGGSCACAGATCCTGGGCTCAG	60		
Db				
47	atggcctgggctgtgctctctcctcactcactcactcaggcacagggtctctggggccag	106		
QY 61	TCGCCCGGACTCAGCCTCCCTCTGTGCTGGGTCCTCTGGACAGTCGGTCACCATCTCC	120		

	Query Match	75.7%;	Score 295.2;	DB 5;	Length 1636;
	Best Local Similarity	87.3%;	Pred. No. 1.9e-71;		
	Matches 337;	Conservative 0;	Mismatches 43;	Indels 6;	Gaps 1
Qy	11	CTCTGCTCCTCGTACACCCCTCTCACTCAGGGCACAGGATCTCTGGGCTCAGTCTGCCCCGA	70		
Db	1552	CACTCCTCTTCTCACCCCTCTCTCACTCAGGACACAGGGTCTCTGGGCCCACTCTGCCTCTGA	1493		
Qy	71	CTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCAACCATCTCCTGCACCTGGAA	130		
Db	1492	CTCAACCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCAGTCACCATCTCTGCACCTGGAA	1433		
Qy	131	CCAGCGATGACGTTGGTGGTTATATACTATGCTCTCTGTTACCAACACCCAGGCCAAAG	190		
Db	1432	CCAGCGATGCTGTTGGGAATTATAACTTTGTCTCTGTTACCAAGACACCCAGGCCAAAG	1373		

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OY 191 CCCCCAACTCATGATTTATGATGTCGTAAAGCGGGCCTCAGGGGTCTCTGATCGCTTCT 250
|||||
Db 1372 CCCCCAACTCCTGATTTATGAGTCAAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCT 1313
|||||
OY 251 CTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 310
|||||
Db 1312 CTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 1253
|||||
OY 311 AGGCTGATTACTGTTGTTTCATATAACACAGTAGCATTGTGTTA-----TTTCGAA 364
|||||
Db 1252 AGGCTGATTACTGACCTCATACACAGCAGCAGCAGTGTGTTGTTCTTCGGAA 1193
|||||
OY 365 GAGGACCGGTTGACCGTCTAGGT 390
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Db 1192 CTGGACCAAGGTACCGTCTAGGT 1167
|||||

RESULT 14
US-09-785-276A-28418/c
; Sequence 28418, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28418
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-28418

Query Match 75.7%; Score 295.2; DB 5; Length 1636;
Best Local Similarity 87.3%; Pred. No. 1.9e-71;
Matches 337; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

OY 11 CTCGTGCTCTGTCACCTCTCCTCACTCAGGGCACAGGATCTCTGGGCTCAGTCTGCCCGCA 70
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Db 1552 CACTCTCTCTCTCCTCCTCCTCACTCAGGACACAGGGTCTCTGGGCCAGTCTGCCCTGA 1493
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OY 71 CTCAGCTCCCTCTGCTGCTGGTCTCCTGGACAGTCTGGTCACTCTCTGCTGCTGGA 130
|||||
Db 1492 CTCACCTGCCCTGGTCTGGGTCCTCTGGACAGTCTGCTGCTGCTGCTGCTGCTGCTG 1433
|||||
OY 131 CCAGCGTACGCTGTTGGTGTATACTATGCTCTGCTGGTACCAACACACCCAGGCAAG 190
|||||
Db 1432 CCAGCGATCTGTTGGGATTTATACTTTGCTCTGCTGGTACCAAGACACCCAGGCAAG 1373
|||||
OY 191 CCCCCAACTCATGATTTATGATGTCGTAAAGCGGGCCTCAGGGGTCTCTGATCGCTTCT 250
|||||
Db 1372 CCCCCAACTCCTGATTTATGAGTCAAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCT 1313
|||||
OY 251 CTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 310
|||||
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Db 1312 CTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 1253
|||||
OY 311 AGGCTGATTACTGTTGTTTCATATAACACAGTAGCATTGTGTTA-----TTTCGAA 364
|||||
Db 1252 AGGCTGATTACTGACCTCATACACAGCAGCAGCAGTGTGTTGTTCTTCGGAA 1193
|||||
OY 365 GAGGACCGGTTGACCGTCTAGGT 390
|||||
Db 1192 CTGGACCAAGGTACCGTCTAGGT 1167
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RESULT 15
US-09-918-995-16199
; Sequence 16199, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16199
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(413)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-16199

Query Match 73.8%; Score 288; DB 5; Length 413;
Best Local Similarity 84.4%; Pred. No. 1.4e-69;
Matches 324; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

OY 1 ATGGGCTGGACTCTGCTCCTCGTCACCCCTCCCTCACTCAGGGCACAGGATCTCTGGGCTCAG 60
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Db 29 atggctgggctctgctctattctccacctctcactcaaggcacagggctcctgggcccag 88
|||||
OY 61 TCTGCCCCACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCACTCATCTCC 120
|||||
Db 89 tctgcctgaactcagcctgcctccgtgtctgggtctcctggagcagtcgatcaccatctcc 148
|||||
OY 121 TGCACCTGGAAACGACGATGACGCTGTGGTGTATTAATACTATGTCCTGTGTACCAACACAC 180
|||||
Db 149 tgcactgggaatcagcagtgacgtggtgattataggagtgtctcctcctggcaccactgcac 208
|||||
OY 181 CCAGGCAAAAGCCCCAAACTCATGATTTATGATGTCGCTAAGCGGCCCTCAGGGGTCTCT 240
|||||
Db 209 ccaggcaaaagccccaaagtcataatttatgatgcaatattcggccctcaggggttct 268
|||||
OY 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||
Db 269 aatcgcttctctgctccaaagtcgtgcaaacagggcctcctcctgagcatctctgggctccag 328
|||||
OY 301 GCTGAGGACGAGGCTGATTTATTACTGTTTTCATATACACAGTAGCATTGTGTTATTC 360
|||||
Db 329 gctgaggacaggtgtaattactgagctcatatacaaacaccacacaccccccttat 388
|||||
OY 361 GGAAGAGGACCGGTTGACCGTC 384
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Db 389 gctctcgggaactgggaccaaagtc 412
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Search completed: September 23, 2002, 19:58:38
Job time: 7168 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:07:09 ; Search time 110.65 Seconds
(without alignments)
865.767 Million cell updates/sec

Title: US-09-019-441-1
Perfect score: 390
Sequence: 1 ATGGCTGACTGCTCTCT.....CCGGTTGACGCTCCTAGGT 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	390	100.0	390	3	US-08-803-085-1
2	321.2	82.4	891	3	US-09-049-672A-23
3	319.6	81.9	902	2	US-08-378-939-11
4	275.4	70.6	333	2	US-08-958-201-13
5	273.8	70.2	333	2	US-08-958-201-11
6	239.6	61.4	324	4	US-09-240-274-137
7	234.6	60.2	935	3	US-09-049-672A-20
8	233	59.7	393	1	US-08-305-683A-3
9	225.8	57.9	771	4	US-08-991-789A-241
10	225.8	57.9	771	4	US-09-062-451-241
11	208.8	53.5	312	4	US-09-240-274-138
12	194.8	49.9	396	2	US-08-345-321-3
13	194.6	49.9	711	3	US-08-487-550-9
14	194.6	49.9	895	3	US-09-049-672A-25
15	192.8	49.4	933	4	US-09-079-029-8
16	192	49.2	333	2	US-08-652-816A-27
17	183.2	47.0	774	2	US-08-665-202-4
18	179	45.9	336	4	US-09-240-274-133
19	178.6	45.8	330	4	US-09-240-274-132
20	176.2	45.2	330	1	US-08-199-911-1
21	172.8	44.3	333	2	US-08-477-553A-43
22	169	43.3	330	4	US-09-240-274-134
23	168	43.1	333	1	US-08-264-093-5
24	167.2	42.9	908	4	US-09-273-839A-9
25	164.2	42.1	327	4	US-09-240-274-126
26	164.2	42.1	327	4	US-09-240-274-223
27	164.2	42.1	450	2	US-08-966-316-5

28	162.6	41.7	327	4	US-09-240-274-129	Sequence 129, App
29	161	41.3	327	4	US-09-240-274-128	Sequence 128, App
30	161	41.3	327	4	US-09-240-274-130	Sequence 130, App
31	158.8	40.7	431	2	US-08-345-321-7	Sequence 7, Appli
32	158.2	40.6	342	4	US-09-240-274-131	Sequence 131, App
33	153.6	39.4	327	4	US-09-240-274-124	Sequence 124, App
34	153.2	39.3	919	3	US-09-049-672A-24	Sequence 24, Appl
35	153	39.2	327	4	US-09-240-274-123	Sequence 123, App
36	153	39.2	327	4	US-09-240-274-125	Sequence 125, App
37	150.6	38.6	705	3	US-08-487-550-1	Sequence 1, Appli
38	149	38.2	387	1	US-08-379-072A-20	Sequence 20, Appl
39	149	38.2	387	1	US-08-478-039-109	Sequence 109, App
40	149	38.2	387	1	US-08-481-869-20	Sequence 20, Appl
41	149	38.2	387	1	US-08-476-349A-109	Sequence 109, App
42	149	38.2	387	1	US-08-476-237-16	Sequence 16, Appl
43	149	38.2	387	3	US-08-523-894-3	Sequence 3, Appli
44	149	38.2	702	3	US-08-523-894-5	Sequence 5, Appli
45	147	37.7	312	2	US-08-273-146-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-1
; Sequence 1, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..390
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..390
US-08-803-085-1

Query Match	100.0%;	Score 390;	DB 3;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 3.3e-106;		
Matches 390;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	1	ATGSCCTGGACTCTGCTCCGTCACCCCTCCTCACTCAGGGCACAGATCTCTGGGCTCAG	60	
Db	1	ATGSCCTGGACTCTGCTCCGTCACCCCTCCTCACTCAGGGCACAGATCTCTGGGCTCAG	60	
QY	61	TCTGCCCCGACTCAGCCTCCCTCTGTGCTCTGGGTCTCCTGGACAGTCGGTACCACTTCCT	120	
Db	61	TCTGCCCCGACTCAGCCTCCCTCTGTGCTCTGGGTCTCCTGGACAGTCGGTACCACTTCCT	120	
QY	121	TGCAC TGGAAACCGATGACGTTGGTGGTTATAACTATGTCTCTGGGTACCAACACCAC	180	
Db	121	TGCAC TGGAAACCGATGACGTTGGTGGTTATAACTATGTCTCTGGGTACCAACACCAC	180	
QY	181	CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGGCTAAGCGGGCCCTCAGGGGTCTCT	240	
Db	181	CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGGCTAAGCGGGCCCTCAGGGGTCTCT	240	
QY	241	GATCGCTTCTCTGGCTCCAAGTCTGGCAACAGGGCTCCCTGACCATCTCTCTGGGCTCCAG	300	
Db	241	GATCGCTTCTCTGGCTCCAAGTCTGGCAACAGGGCTCCCTGACCATCTCTCTGGGCTCCAG	300	
QY	301	GCTGAGCAGCAGGCTGATTATTACTGTGTTATATACACCAAGTAGCACTTGTATTTC	360	
Db	301	GCTGAGCAGCAGGCTGATTATTACTGTGTTATATACACCAAGTAGCACTTGTATTTC	360	
QY	361	GGAAGAGGGACCCGGTTGACCGTCTCTAGGT	390	
Db	361	GGAAGAGGGACCCGGTTGACCGTCTCTAGGT	390	

RESULT 2

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US-09-049-672A-23
;
; Sequence 23, Application US/09049672A
; Patent No. 6135941
;
; GENERAL INFORMATION:
;
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
;
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;
; NUMBER OF SEQUENCES: 28
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

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: TELEFAX: 650-845-4166
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: TELEX:
:
: INFORMATION FOR SEQ ID NO: 23:
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: SEQUENCE CHARACTERISTICS:
:   LENGTH: 891 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
: IMMEDIATE SOURCE:
:   LIBRARY: THYRN0T10
:   CLONE: 2872705
: US-09-049-672A-23

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Query Match 82.4%; Score 321.2; DB 3; Length 891;
Best Local Similarity 89.0%; Pred. No. 8.5e-86;
Matches 347; Conservative 0; Mismatches 43; Indels 0

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RESULT      3
US-08-378-939-11
; Sequence 11, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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;/ TITLE OF INVENTION: materials and methods
;/ NUMBER OF SEQUENCES: 23
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
;/ STREET: 6300 Sears Tower, 233 South Wacker Drive
;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60606-6402
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/958,201
;/ FILING DATE:
;/ PRIORITY APPLICATION DATA:
;/ APPLICATION NUMBER: US 60/028,897
;/ FILING DATE: 21-OCT-1996
;/ INFORMATION FOR SEQ ID NO: 11:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 333 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ IMMEDIATE SOURCE:
;/ CLONE: D12 (light chain)
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: 1..333
;/ US-08-958-201-11

Query Match 70.2%; Score 273.8; DB 2; Length 333;
Best Local Similarity 88.9%; Pred. No. 6e-72;
Matches 296; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 58 CAGTCGCCCCGACTCAGCCTCCCTCTGTCTGTGGGTCTCCTGGACAGTCGGTCAACATC 117
Db 1 CAGTCGCTGACTGAGCTGCTCTGTCTGTGGGTCTCCTGGACAGTCGATCACCATC 60

QY 118 TCCTGCACTGGACAGCAGTACGTGGTGGTTTAACTATGTCTCCTGGTACCAACAC 177
Db 61 TCCTGCACTGGACAGCAGTACGTGGTGGTTTAACTATGTCTCCTGGTACCAACAG 120

QY 178 CACCAGGCAAAACCCCAACATCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 237
Db 121 CACCAGGCAAAACCCCAACATCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 180

QY 238 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGCCCTCCCTGACCATCTCTGGGCTC 297
Db 181 CTAATCGCTTCTCAGGCTCCAAAGTCTGGCAACACAGCCCTCCCTGACCATCTCTGGGCTC 240

QY 298 CAGGCTGAGCAGAGCTGATTATTACTGTTGTCATATACACAGTAGCATTGTTTA 357
Db 241 CAGGTTGAGCAGAGCTGATTATTACTGAGCTCACTTACACGAGTCACTGTGATC 300

QY 358 TTCCGAAGAGACCCGGTTGACCGTCCTAGGT 390
Db 301 TTCCGCGGAGGACCAAGCTGACCGTCTAGGT 333

RESULT 6
US-09-240-137
; Sequence 137, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274

;/ CURRENT FILING DATE: 1999-01-29
;/ EARLIER APPLICATION NUMBER: 60/081,380
;/ EARLIER FILING DATE: 1998-04-10
;/ EARLIER APPLICATION NUMBER: 60/028,550
;/ EARLIER FILING DATE: 1996-10-11
;/ NUMBER OF SEQ ID NOS: 224
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 137
;/ LENGTH: 324
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ OTHER INFORMATION: anti-Rh(D) chain R01
;/ US-09-240-274-137

Query Match 61.4%; Score 239.6; DB 4; Length 324;
Best Local Similarity 86.8%; Pred. No. 7.4e-62;
Matches 276; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 70 ACTCAGCCTCCCTCTCTGTCTGTGGGTCTCCTGGACAGTCGGTCAACATCTCCTGCACTGGA 129
Db 10 actcagctccctcccgctccgggtctctcggacagtcagtcacctctctcgcactgga 69

QY 130 ACCAGCGATGACGTTGGTGGTTATATACTATGTCTCTGTGTACCAACACCAACAGGCAAA 189
Db 70 gccagcagtgagtggtgcttataagcagctctcctctgttaccacaacacccagcaaa 129

QY 190 GCCCCCAAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTCTCTGATCGCTTC 249
Db 130 gcccccaaaactcctgactcatgagggcactaaagcgcctcaggggtcctctgctgcttc 189

QY 250 TCTGGCTCCAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGCTCCAGGCTGAGGAC 309
Db 190 tctggctcaagctctggcaacagcgctccctgacgctctctggtccaggtcaggtat 249

QY 310 GAGGCTGATTATTACTGTTGTTTCATATACACAGTAGCATTGTTATTTCGGAAGAGGG 369
Db 250 gaggctgattattactgcagctcatttga---ggLaattccgtgatatttcggcgaggg 306

QY 370 ACCCGGTTACCGTCCCTA 387
Db 307 accaagctgaccgtccta 324

RESULT 7
US-09-049-672A-20
; Sequence 20, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

Db 274 GACCGATCTCTGGCTCCAAAGCTGGCACTCAGCCCTCCCTGCCCATCAGTGGGCTCCGG 333
QY 301 GCTGAGCAGCAGGCTGATTACTGTTTTCATATACAAACAGT---AGCAGCTTTGTGA 357
Db 334 CCGAGGATGAACACTGATTACTCTGCAACATGGATGACAGTCTCAGTGGTTGATG 393
QY 358 TTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
Db 394 TTCGGCGGAGGACCAAGCTGACCCGTCCTAGGT 426

RESULT 15

US-09-079-029-8
; Sequence 8, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilia W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 933 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-09-079-029-8

Query Match 49.4%; Score 192.8; DB 4; Length 933;
Best Local Similarity 74.1%; Pred. No. 6.7e-48;
Matches 258; Conservative 0; Mismatches 87; Indels 3; Gaps 1;
QY 46 GGATCTGGGCTCAGTCTGCCCGACTACGCTCCCTCTGTCTGGGTCTCCTGGACAG 105
Db 505 GGTGGCGGATCGCAGTCTGTGTGACGAGCGCCCTCAGTGTCTGGGCCCCCAGGACAG 564
QY 106 TCGGTCAACCATCTCTGCACTTGGAAACCGATGAGGTTGGTGGTTTATAACTATGTCTCC 165
Db 565 AGGTCACCATCTCTCTGCACTGGGAGAAGCTCCAACATCGGGCAGGTCTATGATGTACAC 624
QY 166 TGTACCAACACCCAGGCAAGCCCAACTCATGATTTATGATGTCTAGCGG 225
Db 625 TGTACCAACCACTTCCAGGAACAGCCCCCAACTCTCTATGATGACAGCAATCGG 684
QY 226 GCCTCAGGGGTCTCTGATCGTCTCTGCTGCAAGTCTGGCAACACAGGCTCCCTGACC 285

Db 685 CCGTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACTCAGCCTCCCTGGGC 744
QY 286 ATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTTTCATATACAAACAG- 344
Db 745 ATCACTGGGCTCCAGGCTGAAGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGC 804
QY 345 --TAGCAGCTTTGTTATTTCGGAAGAGGAGGCCCGTTGACCGTCTCTAGGT 390
Db 805 CTAGGGGTTCGGTATTTCGGCGGAGGACCAAGGTCACCTGTCCTAGGT 852

Search completed: September 23, 2002, 18:00:46
Job time: 3217 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:50:03 ; Search time 2581.68 Seconds
(without alignments)
3428.746 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGAACACTGTGGTCTT.....TCTGTGTCACCGTCTCCTCA 423

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_nu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	323.8	76.5	420	9	MMU57560	U57560 Macaca mla
2	319	75.4	420	9	MMU57565	U57565 Macaca mla
3	318.2	75.2	411	9	MMU57563	U57563 Macaca mla
4	315.6	74.6	423	9	HSIGHXX28	X55910 H.sapiens m
5	314.6	74.4	414	9	MMU57568	U57568 Macaca mla
6	313.2	74.0	1431	6	AR108867	AR108867 Sequence
7	312.4	73.9	426	9	AF062120	AF062120 Homo sapi
8	311	73.5	420	9	HSIGHXX25	X65907 H.sapiens m
9	310	73.3	420	9	HUMIGHRH	M99607 Human (clon
10	309.8	73.2	468	9	HUMIGHZF	L29122 Human immu
11	305.6	72.2	414	9	HST22X26	Z75399 H.sapiens m
12	305	72.1	414	9	HSIGHXX23	X65905 H.sapiens m
13	303.4	71.7	435	9	MMU57566	U57566 Macaca mla
14	302.8	71.6	423	9	AF174036	AF174036 Homo sapi
15	301.8	71.3	432	9	HSIGHXX26	X65908 H.sapiens m
16	301.2	71.2	423	9	HSIGHXX20	X65902 H.sapiens m
17	299.8	70.9	1404	6	AR135375	AR135375 Sequence
18	299.8	70.9	1404	6	AR135376	AR135376 Sequence
19	299.8	70.9	1404	6	AR135377	AR135377 Sequence
20	299.6	70.8	423	9	AF062258	AF062258 Homo sapi
21	298.6	70.6	423	9	HST14X12	Z75364 H.sapiens m
22	298.2	70.5	423	6	AR008995	AR008995 Sequence
23	298.2	70.5	423	6	I61194	I61194 Sequence 19
24	298.2	70.5	423	6	I78743	I78743 Sequence 19
25	298.2	70.5	453	9	HSE5444	Z14196 H.sapiens r
26	298.2	70.5	2149	9	BC011857	BC011857 Homo sapi
27	297	70.2	423	9	HST14X24	Z75375 H.sapiens m
28	296.6	70.1	429	9	AF062232	AF062232 Homo sapi
29	295.2	69.8	420	6	AR006813	AR006813 Sequence
30	295.2	69.8	420	6	AR135372	AR135372 Sequence
31	295.2	69.8	420	6	I71325	I71325 Sequence 10
32	295	69.7	420	9	AF062220	AF062220 Homo sapi
33	294.8	69.7	423	9	HSIGHXX29	X65911 H.sapiens m
34	294.8	69.7	426	9	AF062278	AF062278 Homo sapi
35	294.6	69.6	416	9	HSIGHXX27	X65909 H.sapiens m
36	292.4	69.1	1431	6	AR108863	AR108863 Sequence
37	292.2	69.1	450	9	HSE554A1	Z14182 H.sapiens r
38	291.8	69.0	417	9	AF062126	AF062126 Homo sapi
39	291.8	69.0	420	9	AF062101	AF062101 Homo sapi
40	291.8	69.0	420	9	AF062196	AF062196 Homo sapi
41	290.2	68.6	426	9	AF062129	AF062129 Homo sapi
42	290.2	68.6	426	9	AF062207	AF062207 Homo sapi
43	290	68.6	423	9	HSIGHXX24	X65906 H.sapiens m
44	290	68.6	456	9	HSIGH239	X67906 H.sapiens r
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ALIGNMENTS

RESULT 1

MMU57560

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

420 bp mRNA linear PRI 11-FEB-1998
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
U57560
U57560.1 GI:1575067
rhesus monkey.
Macaca mulatta
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F.,
Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)
Mol. Immunol. 34 (3), 237-253 (1997)
97368199
2 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.

and Capra, J.D.
Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
FEATURES
Location/Qualifiers
source 1..420
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/organism="Macaca mulatta"
/locus_tag="Macaca mulatta"
/locus="hybridoma 1C8"
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/codon_start=1
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LRSLTAAADTAFFVFCARDGGYSSRFDFWGGVLTVSS"
BASE COUNT 76 a 128 c 121 g 95 t
ORIGIN
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Best Local Similarity 87.0%; Pred. No. 1.6e-78;
Matches 368; Conservative 0; Mismatches 52; Indels 3; Gaps 1;
QY 1 ATGAACACCTGTGGTTCCTCTCTCTGTGTGCAGCTCCAGATGGTGCTGTCCAG 60
Db 1 ATGAACACCTGTGGTTCCTCTCTCTGTGTGCAGCTCCAGATGGTGCTGTCCAG 60
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QY 241 AACCCGTCCCTCAAGATCGAGTCATCATTTCAACAAGACAGCTCCAGACAGATTCTCC 300
Db 241 AACCCCTCCCTCAAGATCGAGTCATCATTTCAATAGACACAGCTCCAGACAGATTCTCC 300
QY 301 CTGAACCTGAACCTCTGTGACCGCGCGACACGCCCTGTATTACTGTGCAGAGATTGG 360
Db 301 CTGAACCTGTGCTCTGTGACCGCGCGACACGCCCTGTATTACTGTGCAGAGATTGG 360
QY 361 GCCCAATAGTGGAAACAACAGCTAGGCTTCTGGGGCCAGGAGTCCCTGGTCCAGCTCC 420
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QY 421 TCA 423
Db 418 TCA 420
RESULT 2
MMU57565
LOCUS
DEFINITION
Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
rhesus monkey.
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecoidea; Macaca.
REFERENCE
1 (bases 1 to 420)

ACCESSION	U57563
VERSION	U57563.1 GI:1575073
KEYWORDS	.
SOURCE	rhesus monkey.
ORGANISM	Macaca mulatta
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopithecinae; Macaca. 1 (bases 1 to 411)
AUTHORS	Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.
TITLE	Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34) Mol. Immunol. 34 (3), 237-253 (1997)
JOURNAL	97368199
MEDLINE	
AUTHORS	2 (bases 1 to 411)
TITLE	Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A. and Capra,J.D.
JOURNAL	Direct Submission
FEATURES	Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Bldv., Dallas, TX 75235-9140, USA Location/Qualifiers
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ORIGIN	81 a 124 c 115 g 91 t
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Best Local Similarity	88.2%; Pred. No. 5.4e-77;
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Qy	61 CTGCACTGCAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCAC 120
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Db	121 TGCGTGCTCTGTGGGCTC---CATCAGCAGTAACACTGGAGCTGGATCCGCCAGCC 177
Qy	181 CCAGGAAGGACCTGGAGTGGAGCTATCTCTGTGTGGTGGTGGGCCACCACAATAC 240
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Qy	361 GCCCAAATAGCTGAACAACGCTAGGCTTCTTGGGGCCAGGGAGTCCCTGGTCACCGTCTCC 420
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LOCUS
DEFINITION H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8).
ACCESSION X65910.1 GI:395108
VERSION    X65910.1
KEYWORDS   diversity region; Ig heavy chain; immunoglobulin; joining region;
           variable region.
SOURCE
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 423)
            Schif, C.
            Direct Submission
            Submitted (08-APR-1992) C. Schif, Centre D'Immunologie de
            Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
REFERENCE  2 (bases 1 to 423)
            Millil, M., Le Deist, F., de Saint-Basile, G., Fischer, A.,
            Fougereau, M. and Schif, C.
            Bone marrow cells in X-linked agammaglobulinemia express
            pre-B-specific genes (lambda-like and V pre-B) and present
            immunoglobulin V-D-J gene usage strongly biased to a fetal-like
            repertoire
            J. Clin. Invest. 91 (4), 1616-1629 (1993)
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                     /cell_type="pre-B"
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Query Match      74.6%; Score 315.6; DB 9; Length 423;
Best Local Similarity 87.1%; Pred. No. 2.8e-76;
Matches 371; Conservative 0; Mismatches 49; Indels 6; Gaps 2;

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Qy  121 TGCCTGTCTCTGTGGCTCTGTACGACAGTAGTAACCTGGTGGACCTGGATCCGCCAGCCCC 180
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Db  121 TGCCTGTCTCTGTGGCTCTGTACGACAGTAGTAACCTGGTGGAGTTGGGTTCGCCAGCCCC 180
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Qy  181 CCAGGGAAGGACCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC 240
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Db  181 CCAGGGAAGGCGCTGGAGTGGATTGGGAAATCTATCATA--GTGGGAGCACCAACTAC 237
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Qy  241 AACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACAGACGTCCCAAGAACCACTTCTCC 300
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Qy	361	GCCCAATAGCTGCACAA-----CCCTAGGCTTCTGGGGCCAGGAGTC	405
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Db	421	CTGGTCACCGTCTCCCTCA	438

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AF062120	
LOCUS	426 bp mRNA linear PRI 08-MAY-2001
DEFINITION	Homo sapiens clone 2lu-39 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.
ACCESSION	AF062120
VERSION	AF062120.1 GI:1170702

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 426)
AUTHORS Wang, X. and Stollár, B. D.
TITLE Immunoglobulin VH gene expression in human aging
JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)

PUBMED 10527689
REFERENCE 2 (bases 1 to 426)
AUTHORS Wang, X. and Stollar, B.D.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES Location/Qualifiers
source 1..426

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/db_xref="taxon:9606"
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CDS
19...>426
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BASE COUNT								
ORIGIN								

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Oy	73.9%;	Score 312.4; DB 9;	Pred. No. 2.1e-75;	0;	0;	51;	6;	60
	1 ATGAAACACCTGTGGTTCTTCTCCTCTGGTGGCAGCTCCACAGATGGGTCTGTCTCCAG 60							
Ds	78.6%;	Score 312.4; DB 9;	Pred. No. 2.1e-75;	0;	0;	51;	6;	60
	1 ATGAAACACCTGTGGTTCTTCTCCTCTGGTGGCAGCTCCACAGATGGGTCTGTCTCAG 60							

Db 61 GTGCAGCTGCAGGAGTCGGGCCCCAGGACCTGGTGAGCCCTTCGGGGACCCCTGTCCCTCACC 120

QY	121	TGGCGTCTCTCGTCTGCTCTGCACGAGTAGTAAC	TGGTGGACCTCGGATCCGCCAGCCC	180
Db	121	TGGCGTCTCTCTCGTCTGCTCCATCAGCAGTAGTAAC	TGGTGGTCCGCCAGCCC	180
QY	181	CCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTG	TAGTGGTGGGGCCACCAACTAC	240
Db	181	CCAGGGAAGGGCTGGAGTGGATTGGGGAATCTAT	CATA--GTGGGAGCACCACACTAC	237
QY	241	AACCCGTCCTCAGAGTGCAGTCAATCTCACAAGAC	ACAGTCCCAAGACGATTCCTCC	300
Db	238	AACCCGTCCTCAGAGTGCAGTCAATCTCAGACAG	TATCATGACAAAGTCCCAAGACGATTCCTCC	297
QY	301	CTGAACCTGAACTCTGTGACCGCGCGGACACGSC	CGCTGTATTACTGTGCCAGAGATTGG	360
Db	298	CTGAAGCTGAGCTGTGTGACCGCGCGGACACGSC	CGTGTATTACTGTGGCAGAGGCGCC	357
QY	361	GCCCAATAGCTGGAACAAG--CTAGGCTCTCGGG	CGCAGGAGTCTTGTCACCGTC	417
Db	358	CCGACTACCGTGCTACTACAGGTACTTTGACTAC	TGGGGCCAGGGAACCCCTGGTCACCGTC	417
QY	418	TCCTCA	423	
Db	418	TCCTCA	423	

RESULT 8
 HSHGHXX25
 LOCUS
 HSHGHXX25
 DEFINITION
 H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-5).
 ACCESSION
 X65907.1
 VERSION
 X65907.1
 GI:395105
 KEYWORDS
 diversity region; Ig heavy chain; immunoglobulin; joining region;
 variable region.
 SOURCE
 human

REFERENCE
AUTHORS
TITLE
JOURNAL
NUMBER

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
Schiff, C.
Direct Submission
Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de
Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
2

TITLE Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
J. Clin. Invest. 91 (4), 1616-1629 (1993)
J3232287
JOURNAL
MEDLINE

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source
I. .420
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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misc_feature	58	.352	/note="variable region"
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BASE COUNT	84	a 123	c 127 g 86 t

Query Match	73.5%;	Score 311;	DB 9;	Length 420;
Best Local Similarity	85.1%;	Pred. No. 5.2e-75;		

[illegible]

AUTHORS	Fang, Q., Kannapell, C.C., Gaskin, F., Solomon, A., Koopman, W.J. and Fu, S.M.
TITLE	Human rheumatoid factors with restrictive specificity for rabbit immunoglobulin G: auto- and multi-reactivity, diverse VH gene segment usage and preferential usage of V lambda IIIB
JOURNAL	J. Exp. Med. 179, 1445-1456 (1994)
MEDLINE	94216813
FEATURES	Location/Qualifiers
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CDS	/db_xref="taxon:9606"
	/map="14q32.33"
	/cell_line="KES 643"
	/cell_type="non-T"
	/tissue_type="peripheral blood"
	1. .468
	/gene="IGH@"
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	/gene="IGH@"
	/codon_start=1
	/product="immunoglobulin heavy chain VDJ region"
	/protein_id="AAA20138.1"
	/db_xref="GI:465145"
	/translation="MKHLWFFLLVAAPRWLSOVLOQESGCLVKPSTLSLTCAVSGSISSSNWSWVROPKGLGELIYHSGSTNPNPSIKSRVTSVDRSKNQFSLKLSVVTADTAVTYICARGHSSWAFDVGQGLTVTVSSGSASAP"
BASE COUNT	93 a 138 c 139 g 98 t
ORIGIN	
Query Match	73.2%; Score 309.8; DB 9; Length 468;
Best Local Similarity	86.8%; Pred. No. 1.1e-74;
Matches	367; Conservative 0; Mismatches 47; Indels 9; Gaps 2;
QY	1 ATGAACACCTGTGGTTCCTCCTCCTCGTGGCAGCTCCACAGATGGGTCTGTCCACG 60
Db	
QY	38 ATGAACACCTGTGGTTCCTCCTCCTCGTGGCAGCTCCACAGATGGGTCTGTCTCAG 97
Db	
QY	61 CTGCAGCTGCAGGAGTCGGCCCGCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTCAC 120
Db	
QY	98 GTGCAGCTGCAGGAGTCGGGCCCGCAGGACTGGTGAAGCCTTCGGGGACCCCTGTCCCTCAC 157
QY	121 TGGCCTCTCTCTGGTGGCTCTGTGCAGCAGTAGTAACCTGGTGGACCTGGATCCGCCACCC 180
Db	
QY	158 TGGCCTGTCTCTGGTGGCTCCATCAGCAGTAGTAACCTGGTGGAGTTGGGTCCGCCACCC 217
QY	181 CCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC 240
Db	
QY	241 AACCCGTCCTCAAGAGTCAGAGTCATCATTTCAAGACACACGTCCTCAAGAACCAAGTCTCC 300
Db	
QY	275 AACCCGTCCTCAAGAGTCAGAGTCACCATATCAGTAGACAAGTCCCAAGAACCAAGTCTCC 334
QY	301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCCTGTATTACTGTGCAGAGATTGG 360
Db	
QY	335 CTGAAGCTGAGCTGTGTGACCGCGCGGACACGCGCCTGTATTACTGTGGGAGA----- 388
QY	361 GCCCAATAGCTGGAAACACGCTAGGCTTCCTGGGGCAGGAGTCCCTGGTACCCTCTCC 420
Db	
QY	389 GGGCATAGCAGCAGCTGGGCGTTTGACTACTGGGGCCAGGAAACCCCTGGTACCCTCTCC 448
QY	421 TCA 423
Db	
QY	449 TCA 451
RESULT 11	
HST22X26	
LOCUS	HST22X26 414 bp mRNA linear PRI 30-APR-1997
DEFINITION	H. sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T22.26).
ACCESSION	275399


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/tissue_type="bone marrow"
/cell_type="pre-B"
/clone_lib="LE library"
/clone="LE 4-56"
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misc_feature 58..352
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misc_feature 353..382
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misc_feature 383..432
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BASE COUNT 88 a 126 c 123 g 95 t
ORIGIN
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Query Match      71.3%; Score 301.8; DB 9; Length 432;
Best Local Similarity 84.6%; Pred. No. 1.8e-72;
Matches 368; Conservative 0; Mismatches 52; Indels 15; Gaps 2;

Qy 1 ATGAACACCTGTGGTTCTTCTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCAG 60
Db 1 ATGAACACCTGTGGTTCTTCTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCTCAG 60

Qy 61 CTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGAGACCCCTGTCCCTACC 120
Db 61 GTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTTCGGGAGCCCTGTCCCTCAC 120

Qy 121 TGCCTGTCTCTGTGGTCTGTCTCAGCAGTAGTAACCTGTGGACCTCGCCAGGCC 180
Db 121 TGCCTGTCTCTGTGGTCTGTCTCAGCAGTAGTAACCTGTGGAGTTGGTTCGCCAGCCC 180

Qy 181 CCAGGGAAGGGCTGAGTGGATGGACGTATCTCTGTGTAGTGGGGCCACCACCTAC 240
Db 181 CCAGGGAAGGGCTGAGTGGATGGGAAATCTATCATA---GTGGGAGCACCACTAC 237

Qy 241 RACCCGTCCCTCAAGAGTCGAGTCATCATTTACAGACACGTCCAGAACCACTTCTCC 300
Db 238 AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACAAGTCCAGAACCACTTCTCC 297

Qy 301 CTGAACCTGAACCTGTGACCGCCCGGACACGGCCGTATTACTGTGCAGAGATTGG 360
Db 298 CTGAAGCTGAGCTCTGTGACCGCCCGGACACGGCCGTATTACTGTGCAGAACCTAC 357

Qy 361 GCCCAATAGTGG-----AACACGCTAGGCTTCTGGGGCCAGGGAGTCTCTG 408
Db 358 GATATTTTGAAGTGTATTACCACTGACAGTACAACTGGTTCGACCCTGGGGCCAGGAACCTG 417

Qy 409 GTCACCGTCTCTCA 423
Db 418 GTCACCGTCTCTCA 432
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Search completed: September 23, 2002, 17:50:07
Job time: 6861 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:06:45 ; Search time 3874.81 Seconds
(without alignments)
1473.417 Million cell updates/sec

Title: US-09-019-441-2
Perfect score: 423
Sequence: 1 ATGAACACCTGTGGTCTTT.....TCCTGGTCACCGTCTCTCTCA 423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_estha.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estinu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_htc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_htc.*
- 12: gb_gss.*
- 13: em_gss_hum.*
- 14: em_gss_inv.*
- 15: em_gss_pln.*
- 16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301.6	71.3	453	9	AW402337
2	301.4	71.3	862	10	BG397580
3	299	70.7	867	10	BG685428
4	290.2	68.6	798	10	BI771905
5	290	68.6	968	9	AL552672
6	288.4	68.2	850	10	BG685474
7	288.2	68.1	939	9	AL541900
8	285.4	67.5	820	10	BI770055
9	285	67.4	680	10	BG684306
10	283.2	67.0	814	10	BG685325
11	281	66.4	736	10	BG685592
12	280.6	66.3	648	10	BM008069
13	280.4	66.3	643	9	AU134293
14	280	66.2	729	10	BG548421
15	279.6	66.1	570	10	BG684621
16	279.6	66.1	894	10	BG757611
17	279.4	66.1	959	10	BG757666

18	279	66.0	633	10	BG685695
19	278.6	65.9	661	10	BG686421
20	278.4	65.8	416	10	BG757951
21	277.8	65.7	948	10	BM007780
22	277.6	65.6	971	9	AL560682
23	277.4	65.6	632	10	BG341565
24	276.4	65.3	828	10	BG974568
25	276	65.2	980	10	BG684861
26	274.8	65.0	924	10	BG758027
27	273.4	64.6	524	10	BG684700
28	271.8	64.3	733	10	BM008087
29	270.8	64.0	889	10	BG758751
30	270.4	63.9	832	9	AU122174
31	269.4	63.7	1097	10	BF974768
32	269.2	63.6	558	10	BM007652
33	269	63.6	649	10	BG757507
34	268.6	63.5	841	10	BG397667
35	268.4	63.5	742	10	BG745613
36	267.8	63.3	791	10	BG685529
37	267.4	63.2	721	10	BG686995
38	267.4	63.2	937	10	BF663511
39	267	63.1	509	9	AW406349
40	267	63.1	834	10	BG758193
41	266.8	63.1	863	10	BM007811
42	266.4	63.0	809	10	BG685383
43	266.2	62.9	803	10	BG397978
44	265.8	62.8	844	10	BI489640
45	265.2	62.7	859	10	BG757166

ALIGNMENTS

RESULT

AW402337

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW402337 453 bp mRNA linear EST 16-FEB-2000
UI-HF-BK0-aal-g-02-0-UI.rl NIH_MGC_35 Homo sapiens cDNA clone
IMAGE:3053955 5', mRNA sequence.

AW402337
GI:6921023

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 453)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

source

1..453

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3053955"

/clone.lib="NIH_MGC_36"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(0.5-1.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonafido, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 88 a 145 c 129 g 91 t

Query Match 71.3%; Score 301.6; DB 9; Length 453;
Best Local Similarity 86.9%; Pred. No. 6.9e-68;
Matches 344; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 28 CTGGTGGACGCTCCAGATGGGCTGTCCAGCTCCAGCTCCAGAGTCCGGCCCGAGCA 87
Db 8 CTGGTGGACGCTCCAGATGGGCTGTCCAGCTCCAGAGTCCGGCCCGAGCA 67
QY 88 GTGGTGAAGCCTTCGAGAGCCCTGTCCCTCACCTGGCTGTCTCTGGTGGCTGTGTCACG 147
Db 68 CTGGTGAAGCCTTCGAGAGCCCTGTCCCTCACCTGGCTGTCTCTGGTGGCTGTGTCACG 127
QY 148 AGTAGTAACCTGGTGGACCTGGATTCGCCAGCCCGCCAGGGAAGGAGCTGGAGTGGATTGGA 207
Db 128 AGTGGTTACTCTCTGGGCTGGATTCGGCAGCCCGCCAGGGAAGGAGCTGGAGTGGATTGGA 187
QY 208 CGTATCTCTGGTAGTGGTGGGCGCCACCACTACACCCGCTCCCTCAAGAGTCGAGTCATC 267
Db 188 AGTATCTATCATATA---GTGGGAGCAGCTACTACACCCGCTCCCTCAAGAGTCGAGTCAC 244
QY 268 ATTTCAAGACACGCTCCAGAACAGATTCTCCCTGAACCTGAACCTGTGACCCGCGCG 327
Db 245 ATATCAGTAGACAGCTCCAGAACAGATTCTCCCTGAACCTGAGCTCTGTGAGCCGCGCA 304
QY 328 GACACGGCGGTATTTACTGTGCCAGAGATTGGGCCCAATAGCTGGGAACACAGCTAGGC 387
Db 305 GACACGGCGGTATTTACTGTGCCAGACATACGGGCTATATAGTGGGTACCCCTTTGAC 364
QY 388 TTCTGGGGCCAGGAGTCTCTGTGTCACCGTCTCTCTCA 423
Db 365 TACTGGGGCCAGGAGACCTGTGTCACCGTCTCTCTCA 400

RESULT 2
BG397580 862 bp mRNA linear EST 12-MAR-2001
LOCUS 602438620F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565020 5',
DEFINITION mRNA sequence.

ACCESSION BG397580
VERSION BG397580.1 GI:13291028
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LCM1281 row: g column: 05
High quality sequence stop: 827.

FEATURES
source Location/Qualifiers
1..862
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4565020"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 210 a 262 c 244 g 146 t
ORIGIN

Query Match 71.3%; Score 301.4; DB 10; Length 862;
Best Local Similarity 85.3%; Pred. No. 1e-67; 56; Indels 6; Gaps 2;
Matches 361; Conservative 0; Mismatches 56; Indels 6; Gaps 2;

QY 1 ATGAACACCTGTGGTTCT 60
Db 23 ATGAACACCTGTGGTTCT 82
QY 61 CTCGAGCTCGAGAGTCGGGGCCCGAGAGTGGTAAGCCCTTCGGAGACCTGTCCCTCACC 120
Db 83 CTCGAGCTCGAGAGTCGGGGCCCGAGAGTGGTAAGCCCTTCGGGGACCTGTCCCTCACC 142
QY 121 TCGCGTGTCTCTGTGGCTCTGTCTGACAGCTAGTAACTGTGACCTGGATCCGCCAGCCCC 180
Db 143 TCGCGTGTCTCTGTGGCTCTCATCAGCAGTAACTGTGAGTGGTGGTTCGCCAGCCCC 202
QY 181 CCAGGGAAGGGAGTGGAGTGGATTTGACCTATCTCTCTGTGTGGTGGGGCCCACTAC 240
Db 203 CCAGGGAAGGGAGTGGAGTGGATTTGCGGAAATCTATCATA---GTGGGAGCACCAACTAC 259
QY 241 AACCCGTCCTCAAGAGTCGAGTCATCTTTTCAAGACACAGCTCCAGAGACAGCTCTCTCC 300
Db 260 AACCCGTCCTCAAGAGTCGAGTCATCTTTTCAAGAGACAGCTCCAGAGACAGCTCTCTCC 319
QY 301 CTGAACCTGAACCTGTGTACCCGCGGACGCGGCGGTATTACTGTGCCAGAGATTGG 360
Db 320 CTGAAGCTGAGCTCTGTGACCCGCGGACAGCGCGGTATTACTGTGCGAG---TCTG 376
QY 361 GCCCAATAGCTGGAAACAGCTAGGCTTCTGGGGCCAGGAGTCTGTGTACCGCTCTCC 420
Db 377 GGAGACATCTACTACTACGGTATGAGAGCTCTGGGGCCAGGAGGACCGGTCTCCCTCTCC 436
QY 421 TCA 423
Db 437 TCA 439

RESULT 3
BG685428 867 bp mRNA linear EST 01-MAY-2001
LOCUS 602637281F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764956 5',
DEFINITION mRNA sequence.

ACCESSION BG685428
VERSION BG685428.1 GI:13916825
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 867)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLM1623 row: a column: 21
High quality sequence stop: 637.

FEATURES

Location/Qualifiers
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/clone="IMAGE:4764956"
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF7; Site1: XhoI; Site2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
216 a 263 c 245 g 143 t

BASE COUNT

ORIGIN

Query Match 70.7%; Score 299; DB 10; Length 867;
Best Local Similarity 84.9%; Pred. No. 4.4e-67;
Matches 359; Conservative 0; Mismatches 60; Indels 4; Gaps 2;

QY	1	ATGAACACCTGTGGTTCCTCTCCCTGGTGGAGCTCCAGAGTGGTCTGTGCCACG	60
Db	23	ATGAACACCTGTGGTTCCTCTCCCTGGTGGAGCTCCAGAGTGGTCTGTGCCACG	82
QY	61	CTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTCAC	120
Db	83	GTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTCAC	142
QY	121	TGGCGTGTCTGTGGGCTGTCTCAGCAGTGTACCTGTGTGGACCTGGATCGCCAGCC	180
Db	143	TGGCGTGTCTGTGGGCTGTCTCAGCAGTGTACCTGTGTGGAGTGGTGGCCAGCC	202
QY	181	CAAGGGAAGGAGTGGAGTGGATGGACCTATCTCTGGTGGTGGTGGGCCACCACTAC	240
Db	203	CAAGGGAAGGAGTGGAGTGGATGGAGTGGGGAATCTATCATAGTG--GGAGCACAACTAC	260
QY	241	AACCCGTCCCTCAAGAGTCGAGTCAATTCATCAAGACACAGCTCCAAAGAACAGTTCTCC	300
Db	261	AAGCCGTCCCTCAAGAGTCGAGTCAATTCATCAAGAGTCCAAAGAACAGTTCTCC	320
QY	301	CTGAACCTGAACCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCCAGAGATTGG	360
Db	321	CTGAACCTGAGCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCCAGAGTTGGG	380
QY	361	GCCCAATAGCTGGAACAACAGCTAGGCTTCTGGGGCCAGGAGTCTCTGTACCGTCTCC	420
Db	381	AGCATCTACTACTA--CGGTATGGACGCTGGGGCCAGGAGTCTCTGTACCGTCTCC	438
QY	421	TCA 423	
Db	439	TCA 441	

RESULT

BI771905
LOCUS 603058919F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208197 5',
DEFINITION 798 bp mRNA linear EST 25-SEP-2001
ACCESSION BI771905
VERSION BI771905.1 GI:15763483
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11522 row: f column: 06
High quality sequence stop: 794.

FEATURES

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5208197"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site1: NotI; Site2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
174 a 254 c 212 g 158 t

BASE COUNT

ORIGIN

Query Match 68.6%; Score 290.2; DB 10; Length 798;
Best Local Similarity 83.7%; Pred. No. 8e-65;
Matches 354; Conservative 0; Mismatches 63; Indels 6; Gaps 2;

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QY	61	CTGCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCCCTCAC	120
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Db	145	TGGCGTGTCTGTGGGCTGTCTCAGCAGTGTACCTGTGTGGAGTGGATCGCCAGCC	201
QY	181	CAAGGGAAGGAGTGGAGTGGATGGACCTATCTCTGGTGGTGGTGGGCCACCACTAC	240
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QY	301	CTGAACCTGAACCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCCAGAGATTGG	360
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Db	379	AACCTGCCACGATACAACTGGTTCGACCCCTGGGGCCAGGAGTCTCTGTACCGTCTCC	438
QY	421	TCA 423	
Db	439	TCA 441	

Db	203	CCGCCGGGAAGGACGTGGAGTGGATTGGCGGTATCT---ATACCACTGGGAGCACCAAC	259
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Db	260	TACAACCCCTCCCTCAAGAGTGCAGTCCACCATATCAGTAGACAGTCCAAGAACCACTTC	319
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QY	358	TGGSCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCT	407
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RESULT	7		
AL541900			
LOCUS			
DEFINITION	AL541900 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE007YL07 5 prime	939 bp mRNA linear EST 16-FEB-2001	
ACCESSION			
VERSION	AL541900		
KEYWORDS	AL541900.1 GI:12873414		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 939)		
TITLE	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
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	/clone="CS0DE007YL07"		
	/clone_lib="LTI_FL002_P11"		
	/lab_host="DH10B"		
	/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"		
BASE COUNT	195 a 324 c 243 g 176 t		
ORIGIN			
Query Match	68.1%;	Score 288.2;	DB 9; Length 939;
Best Local Similarity	86.0%;	Pred. No. 2 8e-64;	
Matches	369; Conservative	0; Mismatches	48; Indels 12; Gaps 4;
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Db	73	GTGCAGCTGCAGGAGTCCGGCCACAGGAGTGGTGAAGCCTTCGGAGACCGCTGTCCCTCACC	132
QY	121	TGCGCTGTCTGTGTGGCTCTGTGCAGCAGTAGTAACCTGGTGGACCTGGATCCGCCAGCCC	180
Db	133	TGCACTGTCTGTGTGGCTC---CATCAGTAGTTACTTGGAGCTGGATCCGCCAGCCC	189
QY	181	CCAGGGGAAGGACCTGGAGTGGATTGGACGTATCTCTGGTAGTGTGGGGCCACCACCACTAC	240

Db	394	GAGACCCCTTAATAGTGGGACCTACAGTAAGTTTGACCACCTGGGGCCAGGGAACCTGGTC	453
Qy	412	ACCGTCTCCTCA	423
Db	454	ACCGTCTCCTCA	465
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DEFINITION	602575006F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4703352 5',		
ACCESSION	BG548421	mRNA sequence.	
VERSION	BG548421.1	GI:13547086	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
TITLE	1 (bases 1 to 729)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI541 row: k column: 01 High quality sequence stop: 711. Location/Qualifiers 1. 729 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4703352" /clone_lib="NIH_MGC_77" /lab_host="DH10B (T1 phage-resistant)" /note="organ: lung; Vector: pDNR-LiB (Clontech); Site:1: SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATTTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGGGCGGACATG-DT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
FEATURES	source		
BASE COUNT	141 a 238 c 208 g 142 t		
ORIGIN			
Query Match	66.2%;	Score 280;	DB 10; Length 729;
Best Local Similarity	85.2%;	Pred. No. 3.4e-62;	
Matches	363; Conservative	0; Mismatches	50; Indels 13; Gaps 4;
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Qy	61	CTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC	120
Db	96	CTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCTACTCACC	155
Qy	121	TGCGCTGTCTGTGGTGCTGTCTCAGCAGTAGTACTACTGGTGACCTGGATCGCCAG	177
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QY 61 CTGCAGCTCAGGAGTGGGGCCAGGAGTGTAAAGCCTTCGGAGACCTGTCCCTCACC 120
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QY 121 TCGGTGTCTCTGGTGGTCTCTCAGCAGTAGTAAGTGGTGGACCTGGATCGCCAGCCC 180
Db 171 TCGGTGTCTATGGTGGTCTCTCAGCAGTAGTAAGTGGTGGACCTGGATCGCCAGCCC 227
QY 181 CCAGGAGGAGTGGTGGATGGAGCTATCTCTGTGTAGTGGTGGGCCACCAACTAC 240
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QY 361 GCCCAATAGCTGGAACACGCTAGGCTCTGCGGCCAGGGAGTCTGTGTACCGTCTCC 420
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QY 421 TCA 423
Db 465 TCA 467
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Search completed: September 23, 2002, 17:06:51
Job time: 4510 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:58:36 ; Search time 488.47 Seconds
(without alignments)
1486.795 Million cell updates/sec

Title: US-09-019-441-2
Perfect score: 423
Sequence: 1 ATGAACACCTGTGGTCTT.....TCCTGGTCACCGTCTCTCA 423

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	423	19 AAV33308	Anti-human CD23 6G
2	313.2	74.0	1431	18 AAT62513	Primate anti-hu
3	313.2	74.0	1431	19 AAV35489	Macaque primate
4	313.2	74.0	1431	24 AAS17247	DNA sequence of a
5	301.2	71.2	423	21 AAZ39331	Nucleotide sequenc
6	299.8	70.9	1404	18 AAT62868	Human gamma-4 heav
7	299.8	70.9	1404	18 AAT62869	Human gamma-4E hea
8	299.8	70.9	1404	18 AAT62870	Human gamma-4E he
9	298.2	70.5	420	21 AAZ39335	Nucleotide sequenc

10	298.2	70.5	423	14 AAO35903	Anti-CD4 VH coding
11	298.2	70.5	423	18 AAT91564	Anti-CD4 cynomolgu
12	298.2	70.5	423	19 AAV31428	Anti-CD4 antibody
13	298.2	70.5	423	19 AAV05695	Monkey anti-CD4 he
14	296.4	70.1	619	22 AAS03048	Human diagnostic a
15	295.2	69.8	420	18 AAT95167	Monkey anti-human
16	295.2	69.8	420	18 AAT62865	Monkey anti-CD4 he
17	295.2	69.8	420	19 AAV23760	Anti-CD4 antibody
18	293.8	69.5	496	20 AAZ24416	Human bladder tumo
19	293.4	69.4	417	21 AAA52907	Human LH1238 mono
20	292.4	69.1	1431	18 AAT62510	Primate anti-hu
21	292.4	69.1	1431	19 AAV35485	Macaque primate
22	292.4	69.1	1431	24 AAS17243	DNA sequence of a
23	290	68.6	1634	21 AAZ50012	Human immune syste
24	289.6	68.5	1567	22 AAC66522	Human immune syste
25	287.6	68.0	614	20 AAV86218	EST clone O99. Ho
26	286	67.6	417	21 AAA13938	Human PTHP monocl
27	281.4	66.5	397	20 AAZ24417	Human bladder tumo
28	276.2	65.3	1746	21 AAZ27382	Human IGFAM-2 immu
29	275.6	65.2	348	14 AAO42697	Vh 71-4. Homo sap
30	275.6	65.2	348	14 AAO42699	VH411. Homo sapie
31	275.6	65.2	348	14 AAO42700	VH415. Homo sapie
32	274	64.8	348	14 AAO42701	VH416. Homo sapie
33	273.6	64.7	457	20 AAZ24423	Human bladder tumo
34	273.4	64.6	1507	21 AAO09695	Human immunoglobul
35	272.8	64.5	1431	17 AAT18059	Monoclonal antibod
36	270	63.8	1543	22 AAF97947	Human secreted pro
37	269.6	63.7	408	18 AAT79919	Immunoglobulin rB6
38	269.6	63.7	426	14 AAO49154	F105 rearranged va
39	269.4	63.7	456	21 AAZ24290	Human 5' EST isola
40	269.4	63.7	1644	20 AAZ24434	Human bladder tumo
41	269.2	63.6	459	21 AAZ42288	Human 5' EST isola
42	267.6	63.3	351	14 AAO42702	AD26. Homo sapien
43	266.6	63.0	393	21 AAC98188	Human colon cancer
44	266.2	62.9	403	18 AAT73440	Human immunoglobul
45	266.2	62.9	403	19 AAV39238	Functional gamma t

ALIGNMENTS

RESULT	1
AAV33308	
ID	AAV33308 standard; DNA; 423 BP.
XX	AAV33308;
AC	AAV33308;
DT	18-NOV-1998 (first entry)
XX	
DE	Anti-human CD23 6G5 monoclonal antibody heavy chain variable region DNA.
XX	
KW	Anti-human CD23 6G5 monoclonal antibody; heavy chain variable region;
KW	human CD23; IgE; FcR1/CD23; gamma-1 constant region;
KW	gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW	allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
XX	
OS	Macaca fascicularis
XX	
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 QY 361 GCCCAATAGCTGGAA--CAACGCTAGGCTTCTGGGCGCAGGAGTCTGTCTACCGTCC 417
 Db 358 ggctacggtgcagcaatgatgtctttgattctgtgggcccaggctcagggtcaccgtc 417
 QY 418 TGCTCA 423
 Db 418 tcttca 423

RESULT 6

AAT62868
 ID AAT62868 standard; DNA; 1404 BP.

XX AC AAT62868;

XX DT 18-OCT-1997 (first entry)

XX DE Human gamma-4 heavy chain DNA.

KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;
 KW transplant rejection; HIV; therapy; CE9 gamma 4; ss.

OS Homo sapiens.

XX PN WO9709351-Al.

XX PD 13-MAR-1997.

XX PF 05-SEP-1996; 96WO-US14324.

XX PR 06-SEP-1995; 95US-0523894.

XX PA (IDEC-) IDEC PHARM CORP.

XX PI Hanna N, Newman RA, Reff ME;

XX DR WPI; 1997-201913/18.

XX DR P-PSDB; AAW14925.

XX Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis

XX PS Disclosure; Page 82-84; 155pp; English.

XX CC DNA sequences (AAT62868-70) respectively code for the heavy chain
 CC regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
 CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
 CC mutations. They can be used to provide novel monoclonal and
 CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
 CC gamma-4PE, in which the human IgG4 Fc binding domain framework is

CC combined with the antigen binding domains (see also AAW14922-23) of
 CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
 CC show high affinity to human CD4, have little or no immunogenicity
 CC in humans and show reduced or absence of effector function. They
 CC can be used to treat autoimmune diseases such as rheumatoid
 CC arthritis.

XX SQ Sequence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;

Query Match 70.9%; Score 299.8; DB 18; Length 1404;
 Best Local Similarity 83.5%; Pred. No. 4.5e-68;
 Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

QY 1 ATGAACACCTGTGGTTCCTCTCTCTGGTGGGAGCTCCAGATGGGTCTGTCCCGAG 60
 Db 1 atgaacacctgtggttctctctctctctgtggcagccccagatgggtctgttccacg 60
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 Db 121 tgcagtgctctgtggtccatcagcggtgactattattgttctggatccgcaagtcc 180
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 Db 181 ccagggaaagggactggatggatcgtacatctatgagcgtgggtggggcccaattac 240
 QY 241 AACCGTCCCTCAAGAGTCGAGTGCATCTTTCACAAAGACACAGCTCCAAAGAACAGTTCTCC 300
 Db 241 aatccctccctcaaatcgagtcctcattccaatagacacgtcccaagaacctctctcc 300
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 Db 358 atattgaaatatcttcactggttattatactgggcccaggagtcgtgaccgtctcc 417
 QY 421 TCA 423
 Db 418 tca 420

RESULT 7

AAT62869
 ID AAT62869 standard; DNA; 1404 BP.

XX AC AAT62869;

XX DT 18-OCT-1997 (first entry)

XX DE Human gamma-4E heavy chain DNA.

KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;
 KW transplant rejection; HIV; therapy; CE9 gamma-4E; ss.

OS Homo sapiens.

XX PN WO9709351-Al.

XX PD 13-MAR-1997.

XX PF 05-SEP-1996; 96WO-US14324.

XX PR 06-SEP-1995; 95US-0523894.

XX PA (IDEC-) IDEC PHARM CORP.

XX Hanna N, Newman RA, Reff ME;
 XX WPI: 1997-201913/18.
 DR P-PSDB; AAW14926.
 XX Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis
 XX
 PS Disclosure: Page 86-88; 155pp; English.
 XX
 CC DNA sequences (AAT62868-70) respectively code for the heavy chain
 CC regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
 CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
 CC mutations. They can be used to provide novel monoclonal and
 CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
 CC gamma-4PE, in which the human IgG4 FC binding domain framework is
 CC combined with the antigen binding domains (see also AAW14922-23) of
 CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
 CC show high affinity to human CD4, have little or no immunogenicity
 CC in humans and show reduced or absence of effector function. The
 CC gamma-4E and -4PE mutations confer activity enhanced stability and
 CC eliminate depleting activity. The antibodies can be used to treat
 CC autoimmune diseases such as rheumatoid arthritis.
 XX
 SQ Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;

Query Match 70.9%; Score 299.8; DB 18; Length 1404;
 Best Local Similarity 83.5%; Pred. No. 4.5e-68;
 Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;
 QY 1 ATGAACACCTGTGTTCTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTCTCCAG 60
 Db 1 atgaacacctgtgttctctctctctctctgtggcagccccagatgggtctgtccag 60
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 Db 61 gtgcagctgcagagtcggggccagagctggcagccccagatgggtctgtccag 120
 QY 121 TCGGCTGTCTGTGGTCTCTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTCTCCAG 180
 Db 121 tgcagtgctgtgtgtctctctctctctctgtggcagccccagatgggtctgtccag 180
 QY 181 CCAGGAGAGGAGTGGAGTGGAGTATCTCTGTGTAGTGGTGGGCCACCAACTAC 240
 Db 181 ccaggaggaggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
 QY 241 AACCCGTCCTCAAGAGTCGAGTATCTATTTCAAGACACGTCCAAAGACCAAGTCTCC 300
 Db 241 aatccctccctcaaatcgatgtctctctctctctctctctctctctctctctctcc 300
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 Db 301 ctgaacctgagctgtgaccccgagacagcgcgctctattactgtgcgagtaatt--- 357
 QY 361 GCCCAATAGCTGGAACACGCTAGGCTCTCTGGGCCAGGGAGTCTGTCTACCGCTCC 420
 Db 358 atattgaataatcttcaactgttattactgtggggccaggagtgctgtgtccagctctcc 417
 QY 421 TCA 423
 Db 418 tca 420

RESULT 8

ID AAT62870
 XX AAT62870 standard; DNA; 1404 BP.

AC AAT62870;

XX

DT 18-OCT-1997 (first entry)
 XX Human gamma-4PE heavy chain DNA.
 DE
 XX CD4; monoclonal antibody; chimeric antibody; recombinant antibody;
 KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
 KW leukaemia; lymphoma; graft-versus-host disease; asthma;
 KW transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9709351-A1.
 XX
 PD 13-MAR-1997.
 XX
 PF 05-SEP-1996; 96WO-US14324.
 XX
 PR 06-SEP-1995; 95US-0523894.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Hanna N, Newman RA, Reff ME;
 XX
 DR WPI: 1997-201913/18.
 DR P-PSDB; AAW14927.
 XX
 PT Chimeric antibody comprising monkey variable domains and human
 PT constant domains - affects CD4-mediated immune functions, esp.
 PT useful for treatment of autoimmune disease, e.g. rheumatoid
 PT arthritis
 XX
 PS Disclosure: Page 91-93; 155pp; English.
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 CC mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
 CC mutations. They can be used to provide novel monoclonal and
 CC chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
 CC gamma-4PE, in which the human IgG4 FC binding domain framework is
 CC combined with the antigen binding domains (see also AAW14922-23) of
 CC macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
 CC show high affinity to human CD4, have little or no immunogenicity
 CC in humans and show reduced or absence of effector function. The
 CC gamma-4E and -4PE mutations confer activity enhanced stability and
 CC eliminate depleting activity. The antibodies can be used to treat
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 XX
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 Query Match 70.9%; Score 299.8; DB 18; Length 1404;
 Best Local Similarity 83.5%; Pred. No. 4.5e-68;
 Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;
 QY 1 ATGAACACCTGTGTTCTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTCTCCAG 60
 Db 1 atgaacacctgtgttctctctctctctctgtggcagccccagatgggtctgtccag 60
 QY 61 CTGCAGCTCGAGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCTCCAC 120
 Db 61 gtgcagctgcagagtcggggccagagctggcagccccagatgggtctgtccag 120
 QY 121 TCGGCTGTCTGTGGTCTCTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTCTCCAG 180
 Db 121 tgcagtgctgtgtgtctctctctctctctgtggcagccccagatgggtctgtccag 180
 QY 181 CCAGGAGAGGAGTGGAGTGGAGTATCTCTGTGTAGTGGTGGGCCACCAACTAC 240
 Db 181 ccaggaggaggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 240
 QY 241 AACCCGTCCTCAAGAGTCGAGTATCTATTTCAAGACACGTCCAAAGACCAAGTCTCC 300
 Db 241 aatccctccctcaaatcgatgtctctctctctctctctctctctctctctctcc 300
 QY 301 CTGAACCTGAACCTGTGACCCCGGACAGACGCGCGGTATATCTGTGCCAGAGATTGG 360
 Db 301 ctgaacctgagctgtgaccccgagacagcgcgctctattactgtgcgagtaatt--- 357
 QY 361 GCCCAATAGCTGGAACACGCTAGGCTCTCTGGGCCAGGGAGTCTGTCTACCGCTCC 420
 Db 358 atattgaataatcttcaactgttattactgtggggccaggagtgctgtgtccagctctcc 417
 QY 421 TCA 423
 Db 418 tca 420

CC construction of a recombinant antibody comprising: (i) an Old World
CC monkey Ig antigen-binding region; and (ii) a human or chimpanzee Ig
CC constant region. The hybrid antibodies can be used as passive or
CC active therapeutic agents against human diseases, e.g. B-cell lymphoma,
CC AIDS, autoimmune and inflammatory diseases, transplant rejection or
CC tumours, or for producing therapeutic and diagnostic conjugates.
CC Although evolutionary distant monkeys are used to raise antibodies
CC against human antigens, they are sufficiently similar that they produce
CC antibodies similar to human antibodies, such that when the monkey
CC antibodies are introduced into humans, no host anti-antibody response
CC is stimulated.

XX

SQ Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;

Query Match 70.5%; Score 298.2; DB 19; Length 423;
Best Local Similarity 83.2%; Pred. No. 8.9e-68;
Matches 352; Conservative 0; Mismatches 88; Indels 3; Gaps 1;

QY 1 ATGAACACCCTGTGGTTTCCTCCTCTGCGAGTGCCTCCAGATGGTGCTGTGCCAG 60
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QY 61 CTGCAGCTGCAGGAGTCGGGCCACGAGGTGTGAAGCCTTCGGAGACCCTGTCCCTCAC 120
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QY 181 CCAGGGAAGGACTGCGAGTGGATTGGAGCTATCTCTGTGTGGTGGGGCCACCAACTAC 240
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DB 184 ccagggaaggactggagtggatcgctacatctatggcagtggtgggggccacaattac 243
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QY 421 TCA 423
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DB 421 tca 423

RESULT 14
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ID AAS03048 standard; cDNA; 619 BP.
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AC AAS03048;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human diagnostic and therapeutic (dithp) cDNA sequence #37.
XX
KW Human diagnostic and therapeutic molecule; dithp; gene therapy;
KW thalassemia; cardiovascular disorder; cell proliferative disorder;
KW cancer; neurodegenerative disorder; autoimmune disorder;
KW infectious disorder; inflammatory disorder; developmental disorder;
KW Incyte ID number 4442487dec; antigen recognition molecule; ss.
XX
OS Homo sapiens.
XX
PN WO200121836-A2.
XX
PD 29-MAR-2001.

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Search completed: September 23, 2002, 17:58:42
Job time: 7006 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:47:11 ; Search time 6364.12 Seconds
(without alignments)
1437.993 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423

Sequence: 1 ATGAACACCTGCTGTTCTT.....TCCTGTCACGTCCTCTCA 423

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43599072

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	313.2	74.0	1431	22	US-09-576-424-11
6	304.4	72.0	681	26	US-09-665-486-420
7	304.4	72.0	681	55	US-60-168-599-709
8	303.2	71.7	541	31	US-09-824-559-7148
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38 290.4 68.7 798 23 US-09-604-897-164 Sequence 164, App
39 290.2 68.6 600 26 US-09-665-486-418 Sequence 418, App
40 290.2 68.6 600 55 US-60-168-599-708 Sequence 708, App
41 290 68.6 1605 16 US-09-205-070-16228 Sequence 16228, A
42 290 68.6 1605 17 US-09-340-623-16228 Sequence 16228, A
43 290 68.6 1605 33 US-09-898-888-16228 Sequence 16228, A
44 290 68.6 1605 33 US-09-898-888A-16228 Sequence 6, Appli
45 290 68.6 1634 15 US-09-107-223A-6

ALIGNMENTS

RESULT

US-09-019-441-2
; Sequence 2, Application US/09019441
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiro
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/803,085

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423

FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..423

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match , 100.0%; Score 423; DB 14; Length 423;

Best Local Similarity 100.0%; Pred. No. 1.3e-96;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAACACCTGTGGTTCCTCCCTCCCTGGTGGCAGCTCCAGATGGGTCTGTCTCCAG 60
DB 1 ATGAACACCTGTGGTTCCTCCCTCCCTGGTGGCAGCTCCAGATGGGTCTGTCTCCAG 60
QY 61 CTGCAGCTCAGGAGTCGGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTCACC 120
DB 61 CTGCAGCTCAGGAGTCGGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTCACC 120
QY 121 TCGCGTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGTGTGGACCTGGATCCGCCAGCCC 180
DB 121 TCGCGTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGTGTGGACCTGGATCCGCCAGCCC 180
QY 181 CCAGGGAAGGAGTGGAGTGGATTCGACCTATCTCTGGTAGTGGTGGGCCCAACTAC 240
DB 181 CCAGGGAAGGAGTGGAGTGGATTCGACCTATCTCTGGTAGTGGTGGGCCCAACTAC 240
QY 241 AACCCGTCCTCAAGAGTCGAGTCATCATTTACAAAGACACACGTCCTCAAGAACCACTCTCC 300
DB 241 AACCCGTCCTCAAGAGTCGAGTCATCATTTACAAAGACACACGTCCTCAAGAACCACTCTCC 300
QY 301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTATTACTGTGCGAGAGATTGG 360
DB 301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTATTACTGTGCGAGAGATTGG 360
QY 361 GCCCAANTAGCTGGAAACAGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCC 420
DB 361 GCCCAANTAGCTGGAAACAGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCC 420
QY 421 TCA 423
DB 421 TCA 423

RESULT 2

US-09-292-053-3
; Sequence 3, Application US/09292053
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
; THEREOF AS THERAPEUTICS
; FILE REFERENCE: 23522.0699
; CURRENT APPLICATION NUMBER: US/09/292,053
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 08/803,085
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(423)
; NAME/KEY: CDS
; LOCATION: (1)..(423)
US-09-292-053-3

Query Match
Best Local Similarity 100.0%; Score 423; DB 16; Length 423;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACACCTGTGGTTCCTCCCTCCCTGGTGGCAGCTCCAGATGGGTCTGTCTCCAG 60
DB 1 atgaacacctgtgttccag 60

QY	61	CTGCAGCTCGAGGAGTCGGGCCCGCAGAGTGGTGAAGCCTTCGGAGACCCGTGTCCTCACC	120
Db	61	ctgcagctcgaggagtcggggcccgaggctggctggaagcctcgagaccctgctccctcacc	120
QY	121	TGGCGTGTCTCGGTGGCTCTGTCAGCAGTAGTAACCTGTGGACCTGGATCGCCAGACCC	180
Db	121	tgcgtgtctctggtgctctgtcagcagtagtaactggtgacctggatccgcgcagccc	180
QY	181	CCAGGGAAGGGACTCGAGTGGATTGGACCTATCTCTGGTAGTGGTGGGCCACCAACTAC	240
Db	181	ccagggaaggactggagctggaattggagcgtactctctggtagggtggggccaccacactac	240
QY	241	AACCCGTCCCTCAAGATGTCGAGTCATCTTTCACAAGACACGCTCCAAAGAACAGATTCTCC	300
Db	241	aacccgtccctcaagagtcgagtcacacttcacaagacacgtcccaagaaacagttctccc	300
QY	301	CTGAACCTGAACCTCTGTGACCGCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG	360
Db	301	ctgaacctgaacctctgtaccgcgcggacacgcccgtgtattactgtgtccagagattgg	360
QY	361	GCCCAATAAGCTGGAAACAACGCTAGGCTTCTGGGGCCAGGGAGTCTGTGTACCCGTTCC	420
Db	361	gcccaaatagctggaacaacgctaggcttctggggccaggaggtcctggtcacctgtctcc	420
QY	421	TCA 423	
Db	421	tca 423	

RESULT 3

```

US-08-746-361-6
; Sequence 6, Application US/08746361
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; APPLICANT: HANNA, Nabil
; APPLICANT: BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; TITLE OF INVENTION: INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
; TITLE OF INVENTION: AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,361
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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RESULTS

RESULT 4
 US-09-383-916-11
 ; Sequence 11, Application US/09383916
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Darrell R.
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 ; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/383,916
 ; FILING DATE: 26-AUG-1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/487,550
 ; FILING DATE: 07-JUN-1995


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: APPLICANT: Yu, Jimmy Y.
: APPLICANT: Greenawalt, Lila B.
: APPLICANT: Panzer, Scott R.
: APPLICANT: Roseberry, Ann M.
: APPLICANT: Wright, Rachel J.
: APPLICANT: Chen, Wensheng
: APPLICANT: Liu, Tommy F.
: APPLICANT: Yap, Pierre E.
: APPLICANT: Stockdreher, Theresa K.
: APPLICANT: Amshey, Stefan
: APPLICANT: Fong, Willy T.
: TITLE OF INVENTION: ANTIGEN RECOGNITION
: FILE REFERENCE: PT-0076 US
: CURRENT APPLICATION NUMBER: US/09/665,486
: CURRENT FILING DATE: 2000-09-20
: PRIOR APPLICATION NUMBER: 60/156,297
: PRIOR FILING DATE: 1999-09-24
: PRIOR APPLICATION NUMBER: 60/156,624
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: 60/156,625
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: 60/168,599
: PRIOR FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: 60/168,197
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: 60/168,614
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: 60/168,611
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: 60/168,613
: PRIOR FILING DATE: 1999-12-02
: NUMBER OF SEQ ID NOS: 958
: SOFTWARE: PERL Program
: SEQ ID NO 420
: LENGTH: 681
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: 444854.
US-09-665-486-420

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Query Match	72.0%;	Score	304.4;	DB	26;	Length	681;
Best Local Similarity	85.4%;	Pred. No.	1.4e-66;				
Matches	364;	Conservative	0;	Mismatches	56;	Indels	6;
Gaps	2;						

QY	1	ATGAAACACCTGTGGTTCCTCTCTCTGTGTGGCAGCTCCAGATGGGTCTCTGTGCCAG	60
Db	77	atgaaacacctgtggtctctctctctctctggtgcagctccagatggctctgtctcag	136
QY	61	CTGCAGCTGCAGGAGTCGGGGCCAGGAGTGTGAAGCCCTCGGAGACCCCTGTCCTCTCAC	120
Db	137	gtcgagctgcaggagtcg9ggcccgagctgtgaagccttcgggacctctccctcacc	196
QY	121	TGCCTCTCTCTGTGGTCTGTTCAGCAGTAGTAACCTGGTGACCTGGATCGCCAGGCC	180
Db	197	tgcgctgtctgtggtcccatcagcagtagtaactgtgtgagttggttcgcccagccc	256
QY	181	CCAGGGAAGGACTTGGAGTGGGATTTGGACGTTATCTCTGTGTAGTGTGGGGCCACCACCACTAC	240
Db	257	ccagggaagg9gctggtggtggtatgggaaatctatcata--g9ggagaccacaatttac	313
QY	241	AACCCGTTCCTCAGAGTCGAGTGCATCATTTCCAGACACACGTCCCAAGAACCCAGTTCTTCC	300
Db	314	aacccttccctccaagctcagtcaccatactcagtagacaagtcgaagaccagtcctctcc	373
QY	301	CTGAACCTGAACCTGTGTACCCCGCCGACACGGCCGTGTATTACTGTGCCAGAG--AT	357
Db	374	ctgaggtgacctctgtgaccgcgcgagacacgcctgtgtattattgtgcgagaggatt	433
QY	358	TGGGCCCAATAGCTGTGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCTCTGGTCCACCGTC	417

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Db 434 atggttcggagggttcagctggttagccctcggggccagggaacccctggtcactgct 493
Qy 418 TCCTCA 423
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Db 494 tectca 499

RESULT 7
US-60-168-599-709
: Sequence 709, Application US/60168599
: GENERAL INFORMATION:
: APPLICANT: Hodgson, David M.
: APPLICANT: Lincoln, Stephen E.
: APPLICANT: Russo, Frank D.
: APPLICANT: Spiro, Peter A.
: APPLICANT: Banville, Steve C.
: APPLICANT: Bratcher, Shawn R.
: APPLICANT: Dufour, Gerard E.
: APPLICANT: Cohen, Howard J.
: APPLICANT: Rosen, Bruce
: APPLICANT: Shah, Purvi
: APPLICANT: Chahal, Michael S.
: APPLICANT: Hillman, Jennifer L.
: TITLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES
: FILE REFERENCE: PT-0099 P
: CURRENT APPLICATION NUMBER: US/60/168,599
: CURRENT FILING DATE: 1999-12-01
: NUMBER OF SEQ ID NOS: 737
: SOFTWARE: PERL Program
: SEQ ID NO 709
: LENGTH: 681
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 444854.24
US-60-168-599-709

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Query Match 72.0%; Score 304.4; DB 55; Length 681;
Best Local Similarity 85.4%; Pred. No. 1.4e-66;
Matches 364; Conservative 0; Mismatches 56; Indels 6;

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Db	77	atgaaacacctgtggttctctctctctgtgtgagctccagatgggtcctgtctcag	136
Qy	61	CTGACGCTGCAGGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCCTAC	120
Db	137	gtgcagctgcaggagtcgggccaggagctggtgaagccttcggggacccctgtccctcacc	196
Qy	121	TGGCGCTCTCTCTGGTGGCTGTGCAGCAGTAGTAACCTGTGGACCTCGGATCCGCCACGCC	180
Db	197	tgogctgtctctggtggtctccacacagcagtagtaacttggctggagcttgcgcagagccc	256
Qy	181	CCAGGGAAGGACTTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC	240
Db	257	ccagggaagggtctggaattggattggggaaattctcata---gtgggagaccacaattac	313
Qy	241	AAOCCGTCCTCAAGAGTCGAGTCATCATTTCCACAGACACGTCCCAAGAACCACTGTTCTCC	300
Db	314	aaccctcccccaagagtcagtcaccatatacagtagacaaagtcacaagaaceagttctcc	373
Qy	301	CTGNACCTGAACTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCCACAG---AT	357
Db	374	cttaggctgacctctgtgacccgcgcggacacgcccgttattattgtgcagagagatt	433
Qy	358	TGGSCCCAAATAGCTGGAACAAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTGCACGTC	417
Db	434	atggtttcggggaggggttcactgctggttcgaccccttcgggcccagggaacccctcgctactgtc	493
Qy	418	TCCTCA 423	

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:58:38 ; Search time 662.78 Seconds
(without alignments)
2056.838 Million cell updates/sec

Title: US-09-019-441-2
Perfect score: 423
Sequence: 1 ATGAACACCTGGTCTT.....TCTGGTCACCGTCTCTCA 423

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US05_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	423	7 US-10-103-686-2	Sequence 2, Appli
2	313.2	74.0	1431	5 US-09-758-173-11	Sequence 11, Appl
3	313.2	74.0	1431	5 US-09-526-098-11	Sequence 11, Appl
4	313.2	74.0	1431	5 US-09-948-429B-11	Sequence 11, Appl
5	313.2	74.0	1431	5 US-09-971-631-11	Sequence 11, Appl
6	313.2	74.0	1431	6 US-10-073-138-6	Sequence 6, Appli
7	313.2	74.0	1431	7 US-10-124-807-11	Sequence 11, Appl
8	313.2	74.0	1431	7 US-10-124-905-11	Sequence 11, Appl
9	313.2	74.0	1431	7 US-10-030-390-11	Sequence 11, Appl
10	299.8	70.9	1404	6 US-10-211-357-7	Sequence 7, Appli
11	299.8	70.9	1404	6 US-10-211-357-9	Sequence 11, Appl
12	299.8	70.9	1404	6 US-10-211-357-11	Sequence 11, Appl
13	298.2	70.5	423	5 US-09-850-165-15	Sequence 15, Appl
14	296.4	70.1	619	7 US-10-089-128-37	Sequence 37, Appl
15	295.2	69.8	420	6 US-10-211-357-1	Sequence 1, Appli
16	292.4	69.1	1431	5 US-09-758-173-3	Sequence 3, Appli
17	292.4	69.1	1431	5 US-09-526-098-3	Sequence 3, Appli
18	292.4	69.1	1431	5 US-09-948-429B-3	Sequence 3, Appli
19	292.4	69.1	1431	5 US-09-971-631-3	Sequence 3, Appli
20	292.4	69.1	1431	7 US-10-124-807-3	Sequence 3, Appli
21	292.4	69.1	1431	7 US-10-124-905-3	Sequence 3, Appli
22	292.4	69.1	1431	7 US-10-030-390-3	Sequence 3, Appli
23	290.8	68.7	1431	6 US-10-073-138-2	Sequence 2, Appli
24	290.4	68.7	798	7 US-10-175-525-164	Sequence 164, App
25	285.4	67.5	1610	6 US-10-206-008-190	Sequence 190, App

ALIGNMENTS

RESULT 1

US-10-103-686-2

; Sequence 2, Application US/10103686

; GENERAL INFORMATION:

; APPLICANT: KLOETZER, Mitchell E.

; NAKAMURA, Takehiko

; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/103,686

; FILING DATE: 25-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/803,085

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 423 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..423

; FEATURE:

; NAME/KEY: mat_peptide

; SEQUENCE 348, App

; SEQUENCE 501, App

; SEQUENCE 162, App

; SEQUENCE 21, Appl

; SEQUENCE 16699, A

; SEQUENCE 163, App

; SEQUENCE 35, Appl

; SEQUENCE 125, App

; SEQUENCE 16650, A

; SEQUENCE 4, Appli

; SEQUENCE 124, App

; SEQUENCE 1382, A

; SEQUENCE 620, App

; SEQUENCE 21, Appl

; SEQUENCE 114467,

; SEQUENCE 6460, Ap

; SEQUENCE 20932, A

; SEQUENCE 20398, A

LOCATION: 58...423
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-103-686-2

Query Match 100.0%; Score 423; DB 7; Length 423;
Best Local Similarity 100.0%; Pred. No. 4.3e-97;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGGAGCTCCAGATGGTCTGTCCCAAG 60
DB 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGGAGCTCCAGATGGTCTGTCCCAAG 60
QY 61 CTCGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCCTTCGAGACACCTGTCCCTCACC 120
DB 61 CTCGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCCTTCGAGACACCTGTCCCTCACC 120
QY 121 TCGGCTGTCTGTGGTGGTCTGTGACGAGTAGTAAGTGTGACCTGGATCGCCAGCCCC 180
DB 121 TCGGCTGTCTGTGGTGGTCTGTGACGAGTAGTAAGTGTGACCTGGATCGCCAGCCCC 180
QY 181 CCAGGAAGGAGTGGAGTGGATGGACGTATCTCTGTGTAGTGGTGGGCCCACTACTAC 240
DB 181 CCAGGAAGGAGTGGAGTGGATGGACGTATCTCTGTGTAGTGGTGGGCCCACTACTAC 240
QY 241 AACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCCAAGAACCACTCTCC 300
DB 241 AACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCCAAGAACCACTCTCC 300
QY 301 CTGAACCTGAACCTGTGACCGCGGGGACAGCGCGGTATTACTGTGCCAGAGATTGG 360
DB 301 CTGAACCTGAACCTGTGACCGCGGGGACAGCGCGGTATTACTGTGCCAGAGATTGG 360
QY 361 GCCCAATAGCTGGAACACGCTAGCTTCTGGGGCCAGGAGTCTCTGTGACCGTCTCC 420
DB 361 GCCCAATAGCTGGAACACGCTAGCTTCTGGGGCCAGGAGTCTCTGTGACCGTCTCC 420
QY 421 TCA 423
DB 421 TCA 423

RESULT 2

US-09-758-173-11
Sequence 11, Application US/09758173
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
AND USE THEREOF AS
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,173
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1431
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1431
US-09-758-173-11

Query Match 74.0%; Score 313.2; DB 5; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.1e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGGAGCTCCAGATGGTCTGTCCCAAG 60
DB 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGGAGCTCCAGATGGTCTGTCCCAAG 60
QY 61 CTCGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCCTTCGAGACACCTGTCCCTCACC 120
DB 61 CTCGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCCTTCGAGACACCTGTCCCTCACC 120
QY 121 TCGGCTGTCTGTGGTGGTCTGTGACGAGTAGTAAGTGTGACCTGGATCGCCAGCCCC 180
DB 121 TCGGCTGTCTGTGGTGGTCTGTGACGAGTAGTAAGTGTGACCTGGATCGCCAGCCCC 180
QY 181 CCAGGAAGGAGTGGAGTGGATGGACGTATCTCTGTGTAGTGGTGGGCCCACTACTAC 240
DB 181 CCAGGAAGGAGTGGAGTGGATGGACGTATCTCTGTGTAGTGGTGGGCCCACTACTAC 240
QY 241 AACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCCAAGAACCACTCTCC 300
DB 241 AACCCCTCCCTCAAGAGTCGAGTCATCATTTTCAAGACACAGTCCCAAGAACCACTCTCC 300
QY 301 CTGAACCTGAACCTGTGACCGCGGGGACAGCGCGGTATTACTGTGCCAGAGATTGG 360
DB 301 CTGAACCTGAACCTGTGACCGCGGGGACAGCGCGGTATTACTGTGCCAGAGATTGG 360
QY 361 GCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGGCCAGGAGTCT 405
DB 361 CTTTTCAGTGTGGTGGATGGTTTACAACTGTTTCGATGTTCTGGGGCCGGGAGTCT 420
QY 406 CTGGTCAACCGTCTCTCTCA 423
DB 421 CTGGTCAACCGTCTCTCTCA 438

RESULT 3

US-09-526-098-11
Sequence 11, Application US/09526098
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
AND USE THEREOF AS
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street

Db 121 TGGCGTGTCTCTGGTGGCTCCATCAGCGTGGTATTATGCTGGGCTGGATCCGCCAGCC 180
QY 181 CCAGGAAGGAGTGGAGTGGATGGACATCTCTGTAGTGGTGGGCGCCACCACTAC 240
Db 181 CCGAGGAAGGGCTGGAGTGGATGGGAGTTTCTATAGTAGTAGTGGGAACCACTACTAC 240
QY 241 AACCCCTCCCTCAAGAGTCCGAGTCATCATTTCAACAGACACGTCACCAAGAACCACTCTCC 300
Db 241 AACCCCTCCCTCAAGAGTCAAGTCCACCAATTTCAACAGACACGTCACCAAGAACCACTCTCC 300
QY 301 CTGAAGTCAAGTCTGTACCGCGGGGACACGGCGGTGTATTACTGTGCCAGAGATTGG 360
Db 301 CTGAAGTCAAGTCTGTACCGCGGGGACACGGCGGTGTATTACTGTGTGAGAGATCGT 360
QY 361 GCCCAATAGCTGGACAA-----CGCTAGGCTTCTGGGCGCCAGGAGTC 405
Db 361 CTTTTCAGTGTGGAAAGTTTACAACAACCTGTTTCGATGTCTGGGCGCCGGAGTC 420
QY 406 CTGGTCACCGTCTCCTCA 423
Db 421 CTGGTCACCGTCTCCTCA 438

RESULT 5
US-09-971-631-11
; Sequence 11, Application US/09971631
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/971,631
; FILING DATE: 09-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/383,916
; FILING DATE: 26-AUG-1999
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide

; LOCATION: 1..1431
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-971-631-11

Query Match 74.0%; Score 313.2; DB 5; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.1e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAACACCTGTGGTTCCTCCTCCTGGTGGAGCTCCAGATGGTCTGTCTGTCTCCAG 60
Db 1 ATGAACACCTGTGGTTCCTCCTCCTGGTGGAGCTCCAGATGGTCTGTCTGTCTCCAG 60
QY 61 CTGAGCTCAGAGTCGCGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCTCCCTCACC 120
Db 61 GTGAGCTCAGAGTCGCGGCCAGGAGTGGTGAAGCCCTTCGGAGACCTGTCTCCCTCACC 120
QY 121 TCGCTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGTGTGGACCTGGATCCGCCAGCCC 180
Db 121 TCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGCTGGATCCGCCAGCCC 180
QY 181 CCAGGAAGGAGTGGAGTGGATGGACATCTCTGTAGTGGTGGGCGCCCAACTAC 240
Db 181 CCAGGAAGGAGTGGAGTGGATGGGAGTTTCTATAGTAGTAGTGGGAACCACTACTAC 240
QY 241 AACCCGTCCTCAAGAGTCCGAGTCATCATTTCAACAGACACGTCACCAAGAACCACTCTCC 300
Db 241 AACCCGTCCTCAAGAGTCAAGTCCACCAATTTCAACAGACACGTCACCAAGAACCACTCTCC 300
QY 301 CTGAAGTCAAGTCTGTACCGCGGGGACACGGCGGTGTATTACTGTGCCAGAGATTGG 360
Db 301 CTGAAGTCAAGTCTGTACCGCGGGGACACGGCGGTGTATTACTGTGTGAGAGATCGT 360
QY 361 GCCCAATAGCTGGACAA-----CGCTAGGCTTCTGGGCGCCAGGAGTC 405
Db 361 CTTTTCAGTGTGGAAAGTTTACAACAACCTGTTTCGATGTCTGGGCGCCGGAGTC 420
QY 406 CTGGTCACCGTCTCCTCA 423
Db 421 CTGGTCACCGTCTCCTCA 438

RESULT 6
US-10-073-138-6
; Sequence 6, Application US/10073138
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7
; AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/073,138
; FILING DATE: 13-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,361
; FILING DATE: 08-NOV-1996
; APPLICATION NUMBER: US 08/487,550

```
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-073-138-6

Query Match 74.0%; Score 313.2; DB 6; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.1e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAACACCTGTGGTTCCTCTCCCTGGTGGCAGCTCCAGATGGGTGCTGTCCCGAG 60
Db 1 ATGAACACCTGTGGTTCCTCTCCCTGGTGGCAGCTCCAGATGGGTGCTGTCCCGAG 60
QY 61 CTGCAGCTGCAGGAGTCGGGGCCGAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 61 GTGCAGCTGCAGGAGTCGGGGCCGAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
QY 121 TCGCGTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
Db 121 TCGCGTGTCTCTGGTGGCTCCATCAGCGGTGGTATGGCTGGGGCTGGATCCGCCAGCCC 180
QY 181 CCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACTAC 240
Db 181 CCAGGGAAGGAGCTGGAGTGGATTGGAGTGGTCTATAGTAGTAGTGGGAACACTACTAC 240
QY 241 AACCCGTCCTCAAGAGTCAGTCAATTTTCAACAGACAGCTCCCAAGAACAGTCTCC 300
Db 241 AACCCGTCCTCAAGAGTCAGTCAATTTTCAACAGACAGCTCCCAAGAACAGTCTCC 300
QY 301 CTGAACCTGAACCTCTGTACCGCGCGGACACGCGCGTGTATTACTGTGCGAGATGG 360
Db 301 CTGAACCTGAACCTCTGTACCGCGCGGACACGCGCGTGTATTACTGTGCGAGATGG 360
QY 361 GCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGGCCAGGGAGTC 405
Db 361 CTTTTTTCAGTTGTTGGAATGGTTTACAAACAACTGGTTCGATGTCTGGGGCCGGAGTC 420
QY 406 CTGGTCACCGTCTCCTCA 423
Db 421 CTGGTCACCGTCTCCTCA 438

RESULT 7
US-10-124-807-11
; Sequence 11, Application US/10124807
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
```

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; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
; US-10-124-807-11
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Query Match 74.0%; Score 313.2; DB 7; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.1e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAACACCTGTGGTTCCTCTCCCTGGTGGCAGCTCCAGATGGGTGCTGTCCCGAG 60
Db 1 ATGAACACCTGTGGTTCCTCTCCCTGGTGGCAGCTCCAGATGGGTGCTGTCCCGAG 60
QY 61 CTGCAGCTGCAGGAGTCGGGGCCGAGAGTGGTCAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 61 GTGCAGCTGCAGGAGTCGGGGCCGAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
QY 121 TCGCGTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
Db 121 TCGCGTGTCTCTGGTGGCTCCATCAGCGGTGGTATGGCTGGGGCTGGATCCGCCAGCCC 180
QY 181 CCAGGGAAGGAGCTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACTAC 240
Db 181 CCAGGGAAGGAGCTGGAGTGGATTGGAGTGGTCTATAGTAGTAGTGGGAACACTACTAC 240
QY 241 AACCCGTCCTCAAGAGTCAGTCAATTTTCAACAGACAGCTCCCAAGAACAGTCTCC 300
Db 241 AACCCGTCCTCAAGAGTCAGTCAATTTTCAACAGACAGCTCCCAAGAACAGTCTCC 300
QY 301 CTGAACCTGAACCTCTGTACCGCGCGGACACGCGCGTGTATTACTGTGCGAGATGG 360
Db 301 CTGAACCTGAACCTCTGTACCGCGCGGACACGCGCGTGTATTACTGTGCGAGATGG 360
QY 361 GCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGGCCAGGGAGTC 405
Db 361 CTTTTTTCAGTTGTTGGAATGGTTTACAAACAACTGGTTCGATGTCTGGGGCCGGAGTC 420
QY 406 CTGGTCACCGTCTCCTCA 423
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Db 421 CTGGTCACCGTCTCCTCA 438
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RESULT 8

US-10-124-905-11

; Sequence 11, Application US/10124905

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/124,905

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1431 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1431

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 1..1431

; US-10-124-905-11

Query Match

Best Local Similarity 74.0%; Score 313.2; DB 7; Length 1431;

Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

Qy 1 ATGAACACCTGTGGTTCTTCCTCTCCCTGGTGGCAGCTCCAGATGGGTCTGTCCACG 60

Db 1 ATGAACACCTGTGGTTCTTCCTCTCCCTGGTGGCAGCTCCAGATGGGTCTGTCCACG 60

Qy 61 CTGCAGCTCAGAGTTCGGGGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120

Db 61 GTGCAGCTCAGAGTTCGGGGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120

Qy 121 TCGGCTGTCTGTGGTCTCTCTCAGCTAGTAACTGGTGACCTGGATCGCCAGCCC 180

Db 121 TCGGCTGTCTGTGGTCTCTCAGCTAGTAACTGGTGACCTGGATCGCCAGCCC 180

Qy 181 CCAGGAAGGAGCTGGAGTGGATTTGGACGTATCTCTGGTAGTGGTGGGCCCACTAC 240
|||||
Db 181 CCAGGAAGGAGCTGGAGTGGATTTGGAGTTTCTATAGTAGTGGGAACACTACTAC 240
|||||
Qy 241 AACCCGTCCTCAAGAGTCGAGTCATATTTCCACAGACACGCTCCAAAGAACCACTTCTCC 300
|||||
Db 241 AACCCGTCCTCAAGAGTCGAGTCATATTTCCACAGACACGCTCCAAAGAACCACTTCTCC 300
|||||
Qy 301 CTGAACCTCAACTCTGTGACCGCCGCGGACGCGCGTGTATTACTGTCTCCAGAGATTGG 360
|||||
Db 301 CTGAACCTCAACTCTGTGACCGCCGCGGACGCGCGTGTATTACTGTCTCCAGAGATTGG 360
|||||
Qy 361 GCCCAAAATAGCTGGAACAA-----CGCTAGGCTTCTGGGGCCCGGAGTGC 405
|||||
Db 361 CTTTTCAGTTGTTGGATGTTTACAACTGTTCTGGGGCCCGGAGTGC 420
|||||
Qy 406 CTGGTCACCGTCTCCTCA 423
|||||
Db 421 CTGGTCACCGTCTCCTCA 438
|||||

RESULT 9

US-10-030-390-11

; Sequence 11, Application US/10030390

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/030,390

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1431 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1431

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 1..1431


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Best Local Similarity      83.5%;   Pred. No. 4,9e+66;
Matches    353;   Conservative     0;   Mismatches    67;   Indels       3;   Gaps       1.

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Oy	1	ATGAACACCTGTGGTCTTCCTCCTCCCTGTTGGAGACTGCCAGATCGGCTCCTGCAG	60
Db	1	ATGAACACCTGTGGTCTTCCTCCTCCCTGGTGAGCCCCCAGAATGGGCTGTGCCAG	60
Oy	61	CTGCAGTCGCAGGAGATCGCGCCAGAGAGTGGTAAGCCTTCGGAGACCCTGTCCAC	120
Db	61	GTCGACCTGCAGGAGATCGGGCCAGGACTGTGAAGCCTTCGAAACCTGTCCAC	120
Oy	121	TGCGCTGTCTCTGTGGGCTCTGTGCAGAGTAGTAAGTGGTGAGCACTGGATCCG	180
Db	121	TGCATGTCTCTGTGGGCTCTCATCAGCGGTACTATTATGGTTCTGGATCCGCA	180
Oy	181	CCAGGGAAGGAGCTGGAGTGGATTGAGCTATCTGTGTAGTGGTGGGCGACAATAC	240
Db	181	CCAGGGAAGGAGCTGGAGTGGATCGGCTAATCTATGACAGTGGTGGGCGACAATAC	240
Oy	241	AACCGTCCCTCAAGAGTCAGTCAATCAATTCACAAGACAGCTCCAAGAACAGTCTCC	300
Db	241	AATCCCTCCCTCAAAATGAGTCTTCATTTATAATGACACGCTCCAAGAACTCTTCTCC	300
Oy	301	CTGAACCTGAATCTGTGTGACCGCCGCGACAGCGCGCTATTACTGTGCCAGAGATTGG	360
Db	301	CTGAATAGAGGTCTGTGACCGCCGCGACAGCGCGCTATTACTGTGCCAGATAT---	357
Oy	361	GCCCAATAGCTGGAAACAAGCTTAGGCTTCTGGGCGAGGAGTCCGTCAACCTTCC	420
Db	358	ATATTGAATATCTTCACGTGTTATTATCTGGGCGCAGGAGGACTCTGGTCAACCTTCC	417
Oy	421	TCA 423	
Db	418	TCA 420	

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RESULT 13
US-09-850-165-15
: Sequence 15, Application US/09850165
GENERAL INFORMATION:
APPLICANT: NEWMAN, ROLAND A.
APPLICANT: HANNA, NABIL W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
FILE REFERENCE: 037003-0280614
CURRENT APPLICATION NUMBER: US-09/850,165
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: 09/082,472
PRIOR FILING DATE: 1998-05-21
PRIOR APPLICATION NUMBER: 08/476,237
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/397,072
PRIOR FILING DATE: 1995-04-17
PRIOR APPLICATION NUMBER: 07/912,292
PRIOR FILING DATE: 1992-07-10
PRIOR APPLICATION NUMBER: 07/856,281
PRIOR FILING DATE: 1992-03-23
PRIOR APPLICATION NUMBER: 07/735,064
PRIOR FILING DATE: 1991-07-25
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 423
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: anti-CD4 VH nucleic acid
NAME/KEY: CDS
LOCATION: (4)..(420)
US-09-850-165-15

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Query March 70.58; Score 298.2; DB 5; Length 423;
Best Local Similarity 83.28; Pred. No. 1,1e-65;
Matches 352; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

QY 1 ATGAACACCTGTGGTTCTTCTCCTCCTGTGGACCTCCAGATGGCTGTGCCAG 60
Db 4 atgaacaccctgtgtctctctctctctctctgtgtgagccccagatggtctgtccag 63
QY 61 CTGCAGCTGCAGGAGTGGGGCCAGAGATGCTGAACCTTGGAGACCTGTCCCTACC 120
Db 64 gtgcagctgcagagagcgggcccagagactgttgaagccttcgagaccctgtccctacc 123
QY 121 TGGCGTGTCTGTGGGGCTGTGTACAGTAGTAAGTGTAGTGGATCGGATCGCCAGCC 180
Db 124 tgcagtgctctgtgtgtgtctcatcagcgggtacctatattgtgtctgtatccgcaatcc 183
QY 181 CCAGGGAAGGAGCTGAGTGGATTGGACGTATCTCTGTGTAAGTGGGGCCACCACATAC 240
Db 184 ccagggaagagagcctgagtgatctgctacatctatgtgcaagtgtgtggggcaccatctac 243
QY 241 AACCGTGTCCCTCAGAGAGTGCAGTATCATTTTCACAAGACAGTCCAGAACATTTCTCC 300
Db 244 aatccctccccaacaacacagcttccatctcaatagacacgctccaagaaccttctcc 303
QY 301 CTGAACCTGAACCTGTGTACCGCCGCGAGACAGGCGCGTATTAAGTGTGACAGATTTGG 360
Db 304 ctgaacctgagtgctgtgacccgcgcgagaccgcgcgtctatctactgtgaggaat--- 360
QY 361 GCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCCGTGATCACCGTCTCC 420
Db 361 atattgaatatcttccactgttatctatctatctggtggccagagctcgttccactctcc 420
QY 421 TCA 423
Db 421 tca 423

RESULT 14
US-10-089-128-37
Sequence 37, Application US/10089128
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: HODGSON, David M.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: RUSSO, Frank D.
APPLICANT: SPIRO, Peter A.
APPLICANT: BANVILLE, Steve C.
APPLICANT: BRATCHER, Shawn R.
APPLICANT: DUFOUR, Gerard E.
APPLICANT: COHEN, Howard J.
APPLICANT: ROSEN, Bruce H.
APPLICANT: SHAH, Puri
APPLICANT: CHALUP, Michael S.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: JONES, Anissa L.
APPLICANT: YU, Jimmy Y.
APPLICANT: GREENMALT, Lila B.
APPLICANT: PANZER, Scott R.
APPLICANT: ROSEBERRY, Ann M.
APPLICANT: WRIGHT, Rachel J.
APPLICANT: CHEN, Wensheng
APPLICANT: LIU, Tommy F.
APPLICANT: YAP, Pierre E.
APPLICANT: STOCKREHER, Theresa K.
APPLICANT: AMSHEY, Stefan
APPLICANT: FONG, Willy T.
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1066 PCT
CURRENT APPLICATION NUMBER: US/10/089,128
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/156,294; 60/155,760; 60/155,939; 60/156,565; 60/156,632; 60/167,542; 60/167,522; 60/167,453; 60/167,517;

DB 361 ATATTGAAATATCTTCACCTGCTTATTTATCTGGGGCCAGGAGACTCCTGCTCACCGTCTCC 420

Search completed: September 23, 2002, 19:58:47
Job time: 7177 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 18:00:46 ; Search time 110.65 Seconds
(without alignments)
939.024 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423
Sequence: 1 ATGAACACCTGTGTTCTT.....TCTGTGTCACCTCTCTCA 423

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	423	100.0	423	3	US-08-803-085-2
2	313.2	74.0	1431	3	US-08-487-550-11
3	299.8	70.9	1404	3	US-08-523-894-7
4	299.8	70.9	1404	3	US-08-523-894-9
5	299.8	70.9	1404	3	US-08-523-894-11
6	298.2	70.5	423	1	US-08-379-072A-19
7	298.2	70.5	423	1	US-08-481-869-19
8	298.2	70.5	423	1	US-08-476-237-15
9	295.2	69.8	420	1	US-08-478-039-107
10	295.2	69.8	420	1	US-08-476-349A-107
11	295.2	69.8	420	3	US-08-523-894-1
12	293.4	69.1	1431	3	US-08-487-550-3
13	289.6	68.5	1567	3	US-09-049-672A-17
14	268	63.4	426	2	US-08-480-774A-1
15	266.2	62.9	403	4	US-09-042-353-357
16	266.2	62.9	403	4	US-08-758-417A-205
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18	263.8	62.4	404	4	US-08-758-417A-203
19	257.8	60.9	524	4	US-09-042-353-419
20	257.8	60.9	524	4	US-08-758-417A-219
21	257.8	60.9	4926	4	US-09-042-353-418
22	257.8	60.9	4926	4	US-08-758-417A-268
23	257.6	60.9	413	4	US-09-042-353-351
24	257.6	60.9	413	4	US-08-758-417A-199
25	249.4	59.0	624	3	US-08-545-809A-28
26	247	58.4	402	1	US-08-259-372A-5
27	247	58.4	402	1	US-08-468-671-5

28	243	57.4	800	3	US-08-545-809A-55	Sequence 55, Appl
29	241.4	57.1	840	4	US-09-260-527-4	Sequence 4, Appl
30	239.6	56.6	1212	3	US-08-545-809A-61	Sequence 61, Appl
31	238.2	56.3	650	3	US-08-545-809A-4	Sequence 4, Appl
32	238	56.3	800	3	US-08-545-809A-39	Sequence 39, Appl
33	237.8	56.2	366	1	US-08-360-125-9	Sequence 9, Appl
34	237.8	56.2	366	2	US-08-450-578-9	Sequence 9, Appl
35	237.8	56.2	366	2	US-09-017-628-9	Sequence 9, Appl
36	237.8	56.2	366	2	US-09-014-880-9	Sequence 9, Appl
37	236.6	55.9	622	3	US-08-545-809A-59	Sequence 59, Appl
38	227.2	53.7	1418	4	US-08-793-450-7	Sequence 7, Appl
39	223.6	52.9	631	3	US-08-545-809A-31	Sequence 31, Appl
40	221.2	52.3	687	3	US-08-545-809A-34	Sequence 34, Appl
41	217.6	51.4	372	2	US-08-477-553A-46	Sequence 46, Appl
42	217	51.3	363	2	US-08-477-553A-50	Sequence 50, Appl
43	213.2	50.4	357	2	US-08-652-816A-20	Sequence 20, Appl
44	210	49.6	384	2	US-08-477-553A-49	Sequence 49, Appl
45	209.8	49.6	357	1	US-08-360-125-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-2
; Sequence 2, Application US/08803085
; Patent No. 6011138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: MAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWICKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..423
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..423
; US-08-803-085-2

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:

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?      CITY: Alexandria
?
?      STATE: VA
?
?      COUNTRY: USA
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?      ZIP: 22314-3187
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?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: Floppy disk
?      COMPUTER: IBM PC compatible
?      OPERATING SYSTEM: PC-DOS/MS-DOS
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Db 358 ATATTGAATATCTTCTACTGTTATTATTACTGGGGCCAGGAGTCTGTGACCGTCTCC 417
QY 421 TCA 423
Db 418 TCA 420
RESULT 5
US-08-523-894-11
; Sequence 11, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabli
; APPLICANT: Newman, Roland A.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E
; FEATURE:
; CHROMOSOME/SEGMENT: mutation
; NAME/KEY: CDS
; LOCATION: 1..1404
; NAME/KEY: mat_peptide
; LOCATION: 1..1404
US-08-523-894-11
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Best Local Similarity 83.5%; Pred. No. 3.5e-78;
Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;
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Db 1 ATGAACACCTGTGTCTTCTCCCTCTGCTGTGACGCTCCAGATGGGCTCTGCCAG 60
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Db 61 GTGACGTGACAGAGTGGGGCCAGAGAGTGTGAAGCTTCGAGACCCGTCCCTAC 120
QY 121 TGGCGTGTCTGTGTGCTGTGTGACGAGTAACTGTGTGACCTGTGATCCGACGCC 180
Db 121 TGGAGTGTCTGTGTGCTGTGTGACGAGTAACTGTGTGACCTGTGATCCGACGCC 180
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QY 241 AACCCGCTCTCAAGAGTGCATCATTTCAACAGACGTCACAAACAGTCTCC 300
Db 241 AATCCCTCTCTCAACATCATCTCATTTCAATAGACAGTCACAAACCTCTCTCC 300
QY 301 CTGAACCTGACCTGTGTGACCGCGGACACGCGCGTGTATTACTGTGCCAGATTGG 360
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QY 361 GCCCAATATACCTGGAACACACGCTAGGCTCTGGGGGCCAGGAGTCTGTGACCGTCC 420
Db 358 ATATTGAATATCTTCTACTGTTATTATTACTGGGGCCAGGAGTCTGTGACCGTCTCC 417
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Db 418 TCA 420
RESULT 6
US-08-379-072A-19
; Sequence 19, Application US/08379072A
; Patent No. 5658570
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, Roland A.
; APPLICANT: HANNA, Nabli
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,072A
; FILING DATE: 25-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 012712-067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620

Query Match	Best local similarity	83.1%	Score 295.2	DB 3:	Length 420:
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RESULT 12

US-08-487-550-3

Sequence 3, Application US/08487550

Query Match	69.1%	Score 292.4	DB 3	Length 1431
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QY	61	CTGCAGCTGCAGGAGTGGGGCCAGAGAGGGGAAGCCTTCGGAGACCTGTGCTCCAC	120	
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QY	121	TGGCGTGTCTGTGGTGCTCTGTCAAGCATGTAACTGTGGACCTGGATCCGCCACCC	180	
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QY	61	CTGCAGCTGCAGAGTCGGGCCAGAGAGTGGTGAAGCTTCGGAGACCTGTCCCTCAC	120
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Dp	400	TCA 402	

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Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-019-441-3

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Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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6: gb_pat:*
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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
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26: em_ro:*
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29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	342.2	88.4	429	9	HUMIGKW	M74019 Homo sapien
2	342.2	88.4	729	6	E40896	E40896 Humanized a
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4	334.2	86.4	396	6	E12918	E12918 Human mRNA
5	332.6	85.9	406	9	HUMIGKFN	M87478 Human reari
6	331.2	85.6	400	9	AF228327	AF228327 Homo sapi
7	330.8	85.5	432	9	HUMIGRVCA	L01279 Homo sapien
8	329.4	85.1	390	9	MM057579	U57579 Macaca mula
9	329.4	85.1	974	6	AX305000	AX305000 Sequence
10	329.4	85.1	974	6	AX306529	AX306529 Sequence
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12	326.2	84.3	396	9	HSPBLIGVD	Z27173 H.sapiens r
13	325.6	84.1	383	9	HSIGKLV56	X72477 H.sapiens r
14	323.6	83.6	389	9	HSIGKLV06	X72427 H.sapiens m
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21	319.4	82.5	399	9	HSIGKLV23	X72444 H.sapiens m
22	318.2	82.2	388	6	ARI61375	ARI61375 Sequence
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25	313.8	81.1	395	9	HSIGKLV41	X72462 H.sapiens m
26	313.4	81.0	388	9	HSDDELIGVJ	X85995 H.sapiens m
27	313.4	81.0	388	9	HSTR0IGVJ	X85996 H.sapiens m
28	313.4	81.0	953	9	BC005332	BC005332 Homo sapi
29	313	80.9	388	9	HSIGKLV58	X72479 H.sapiens m
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33	311.8	80.6	393	9	HUMIG6L	L38434 Homo sapien
34	311.8	80.6	698	6	AX327725	AX327725 Sequence
35	311.8	80.6	944	6	AX067344	AX067344 Sequence
36	310.4	80.2	370	9	HSIGKLV03	X72424 H.sapiens m
37	310.2	80.2	390	9	HSIAM007	Z68958 H.sapiens m
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ALIGNMENTS

RESULT	1	LOCUS	HUMIGKW	DEFINITION	Homo sapiens immunoglobulin light chain variable region (IGLE)	ACCESSION	M74019	VERSION	M74019.1	SOURCE	ORGANISM	human.	REFERENCE	1 (bases 1 to 429)	AUTHORS	Moore,J.S., Nowell,P.C., Roelcke,D., Pruzanski,W., Roudier,J. and Silverman,G.J.	TITLE	Variable region gene analysis of pathologic human autoantibodies to the related I and I red blood cell antigens	JOURNAL	Blood (1991) In press	FEATURES	Location/Qualifiers	1..429	/organism="Homo sapiens"	/db_xref="taxon:9606"

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CRASISISYLMWYQOKREKAKKLITYASSIQSGVPSFSGSGTDTLTITSLQ
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ORIGIN

Query Match 88.4%; Score 342.2; DB 9; Length 429;
Best Local Similarity 92.8%; Pred. No. 2.6e-101;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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DB 1 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGGCTCCAGGTGCC 60
QY 61 AGATGTGACATCCAGATGAGCCAGTCCATCCTCCCTGCTCATCTGTAGAGACAGA 120
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DB 121 GTCACATCATCTGACGGGCAAGTACAGACATTAGTATTAAATTGATACAGAC 180
QY 122 GTACCATCATCTGCGGGGCAAGTACAGACATTAAATTGATACAGAC 180
DB 122 GTACCATCATCTGCGGGGCAAGTACAGACATTAAATTGATACAGAC 180
QY 181 AAACGAGAAAAGCTCTTAAGTCTGTATCTATGTCATCCAGTTGCAAGTGGGGTC 240
DB 181 AAACGAGGAAAGCCCTTAAGTCTGTATCTATGTCATCCAGTTGCAAGTGGGGTC 240
QY 181 AAACGAGGAAAGCCCTTAAGTCTGTATCTATGTCATCCAGTTGCAAGTGGGGTC 240
DB 181 AAACGAGGAAAGCCCTTAAGTCTGTATCTATGTCATCCAGTTGCAAGTGGGGTC 240
QY 241 CCATCAAGGTTTCAGGGGCAAGTATCTGGGACAGATTTCACCTCAGCAGCTG 300
DB 241 CCATCAAGGTTTCAGGGGCAAGTATCTGGGACAGATTTCACCTCAGCAGCTG 300
QY 301 CAGCTGGAAGATTTTGCAGATTATTACTGTCTCAGAGTTATAGTACCCCTCGAGCTTC 360
DB 301 CAGCTGGAAGATTTTGCAGATTATTACTGTCTCAGAGTTATAGTACCCCTCGAGCTTC 360
QY 301 CAGCTGGAAGATTTTGCAGATTATTACTGTCTCAGAGTTATAGTACCCCTCGAGCTTC 360
DB 301 CAGCTGGAAGATTTTGCAGATTATTACTGTCTCAGAGTTATAGTACCCCTCGAGCTTC 360
QY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
DB 361 GGCCAAAGGACCAAGGTGGAATCAAA 387

RESULT 2
LOCUS E40896 729 bp DNA linear PAT 31-JAN-2002
DEFINITION Humanized anti-Fas antibody.
ACCESSION E40896
VERSION E40896.1 GI:18627473
KEYWORDS JP 2000166574-A/85.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 729)
REFERENCE Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
AUTHORS Humandized anti-Fas antibody
TITLE Patent: JP 2000166574-A 85 20-JUN-2000;
JOURNAL SANKYO CO LTD
OS Homo sapiens (human)
COMMENT PN JP 2000166574-A/85

PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
PR NOBURI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKURO TAMAKI
PC C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
PC C07K16/18,
PC C12N1/21,C12N5/10,C12P21/08//C12N1/21,C12N1/19,C12N15/00, PC
C12N5/00
CC
FH Key Location/Qualifiers
FT source 1..729
FT /organism="Homo sapiens (human)"
FEATURES
source Location/Qualifiers
1..729
/db_xref="taxon:9606"

BASE COUNT 192 a 200 c 182 g 155 t
ORIGIN

Query Match 88.4%; Score 342.2; DB 6; Length 729;
Best Local Similarity 92.8%; Pred. No. 2.7e-101;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGGCTCCAGGTGCC 60
DB 7 ATGGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGGCTCCAGGTGCC 66
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DB 61 AGATGTGACATCCAGATGAGCCAGTCCATCCTCCCTGCTCATCTGTAGAGACAGA 126
QY 121 GTCACATCATCTGACGGGCAAGTACAGACATTAGTATTAAATTGATACAGAC 180
DB 121 GTCACATCATCTGACGGGCAAGTACAGACATTAGTATTAAATTGATACAGAC 186
QY 122 GTACCATCATCTGCGGGGCAAGTACAGACATTAAATTGATACAGAC 186
DB 122 GTACCATCATCTGCGGGGCAAGTACAGACATTAAATTGATACAGAC 186
QY 181 AAACGAGAAAAGCTCTTAAGTCTGTATCTATGTCATCCAGTTGCAAGTGGGGTC 240
DB 181 AAACGAGGAAAGCCCTTAAGTCTGTATCTATGTCATCCAGTTGCAAGTGGGGTC 246
QY 187 AAACGAGGAAAGCCCTTAAGTCTGTATCTATGTCATCCAGTTGCAAGTGGGGTC 246
DB 241 CCATCAAGGTTTCAGGGGCAAGTATCTGGGACAGATTTCACCTCAGCAGCTG 300
QY 241 CCATCAAGGTTTCAGGGGCAAGTATCTGGGACAGATTTCACCTCAGCAGCTG 306
DB 241 CCATCAAGGTTTCAGGGGCAAGTATCTGGGACAGATTTCACCTCAGCAGCTG 306
QY 301 CAGCTGGAAGATTTTGCAGATTATTACTGTCTCAGAGTTATAGTACCCCTCGAGCTTC 360
DB 307 CAGCTGGAAGATTTTGCAGATTATTACTGTCTCAGAGTTATAGTACCCCTCGAGCTTC 366
QY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
DB 367 GGCCAAAGGACCAAGGTGGAATCAAA 393

RESULT 3
LOCUS MM057571 390 bp mRNA linear PRI 02-OCT-1996
DEFINITION Macaca mulatta Ig rearranged light chain variable region, anti-RBC
antibody, mRNA, partial cds.
ACCESSION U57571
VERSION U57571.1 GI:1575089
KEYWORDS
SOURCE Rhesus monkey.
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecidae; Macaca.
1 (bases 1 to 390)
REFERENCE Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.
AUTHORS Variable Region Gene Segment Utilization in Rhesus Monkey
TITLE and Capra,J.D.
JOURNAL Hybridomas Producing Human Red Blood Cell-Specific Antibodies:
Predominance of the VH4 Family but not VH4-21 (V4-34)
Unpublished

REFERENCE 2 (bases 1 to 390)
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
 University of Texas Southwestern Medical Center, 6000 Harry Hines
 Blvd., Dallas, TX 75235-9140, USA
 FEATURES
 source
 1. .390
 /organism="Macaca mulatta"
 /db_xref="taxon:9544"
 /note="hybridoma 1D8"
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 /codon_start=1
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 /protein_id="AAB09448.1"
 /db_xref="GI:1575090"
 /translation="MDMRALFQILGLLMLPGARCDIOMTQSPSSLSASVDRTIT
 CRASGISDYNNWYQKPKAPKRLIVASSIESGVPSPFSGSGSTFTLTLSLQ
 EDFATYICLQYNSDPFTGPGTKDKR"
 BASE COUNT 97 a 108 c 94 g 91 t
 ORIGIN
 Query Match 86.4%; Score 334.2; DB 9; Length 390;
 Best Local Similarity 91.5%; Pred. No. 1.1e-98;
 Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGGACATAGAGGCTCCCGCTCAGCTCTCGGGGCTCCTCTGCTGCTGCCAGGTGCC 60
 DB 1 ATGGACATAGAGGCTCCCGCTCAGCTCTCGGGGCTCCTCTGCTGCTGCCAGGTGCC 60
 QY 61 AGATGTGACATCCAGATGACCCAGCTCTCCCTGTCTGACATCTGTAGGGGACAGA 120
 DB 61 AGATGTGACATCCAGATGACCCAGCTCTCCCTGTCTGACATCTGTAGGGGACAGA 120
 QY 121 GTACACATCACTTGGCAGGCAAGTGCAGCATTAAGTATTAATGGTATTCAGCAG 180
 DB 121 GTACACATCACTTGGCAGGCAAGTGCAGCATTAAGTATTAATGGTATTCAGCAG 180
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 DB 181 AAACGAGTAAAGCTCCTAAGCGCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240
 QY 241 CCATCAAGTTTACGCGCAGTGTGATCTGGACAGAGTTCACTCTACCGTCAGCAGCTG 300
 DB 241 CCATCAAGTTTACGCGCAGTGTGATCTGGACAGAGTTCACTCTACCGTCAGCAGCTG 300
 QY 301 CAGCTGAGATTTTGGCACTATTACTGTCTACAGGTTTATAGTACCCTGGAGAGTTC 360
 DB 301 CAGCTGAGATTTTGGCACTATTACTGTCTACAGGTTTATAGTACCCTGGAGAGTTC 360
 QY 361 GGCCAGGAGCAAGGTGAAATCAAA 387
 DB 361 GGCCCGGAGCAAACTGATATCAAA 387
 RESULT 4
 LOCUS E12918 396 bp DNA linear PAT 24-JUN-1998
 DEFINITION Human mRNA for variable region of light chain of anti-carcinoma
 monoclonal antibody CLN'-1-IgM, complete cds.
 ACCESSION E12918
 VERSION E12918.1 GI:3251749
 KEYWORDS JP 1997100300-A/2.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 396)
 AUTHORS Hagihara, H., Aozuka, Y., and Miyahara, J.
 TITLE AMINO ACID SEQUENCE OF ANTICANCER HUMAN MONOCLONAL ANTIBODY AND DNA
 BASE SEQUENCE CODING FOR THE SAME

JOURNAL Patent: JP 1997100300-A 2 15-APR-1997;
 COMMENT HAGIWARA YOSHITIDE
 OS Homo sapiens (human)
 PN JP 1997100300-A/2
 PD 15-APR-1997
 PE 03-OCT-1995 JP 1995278266
 PI HAGIWARA HIDEAKI, AOZUKA YASUYUKI, MIYAHARA JUNICHI PC
 C07K16/42, C07H21/04, C12N15/02, C12N15/09, A61K39/395, C12N5/10, PC
 C12P21/08,
 PC G01N33/53, G01N33/574, G01N33/577;
 CC strandedness: Double;
 CC topology: Linear;
 FH key Location/Qualifiers
 FH source 1. .396
 FT /organism='Homo sapiens'
 FT /cell_type='hybridoma cell'
 FT /cell_line='HT-2'
 FT sig_peptide 1. .66
 FT mat_peptide 67. .396
 FT /product='variable region of light chain of
 FT anti-carcinoma
 FT monoclonal antibody CLN'-1-IgM' FT
 FT misc_feature 136. .168
 FT /note='this region encodes Complementarity FT
 FT determining region (CDR1)'
 FT FT misc_feature 214. .234
 FT /note='this region encodes Complementarity FT
 FT determining region (CDR2)'
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 FT determining region (CDR3)'.
 FEATURES
 source 1. .396
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 101 a 107 c 97 g 91 t
 ORIGIN
 Query Match 86.4%; Score 334.2; DB 6; Length 396;
 Best Local Similarity 91.5%; Pred. No. 1.1e-98;
 Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGGACATAGAGGCTCCCGCTCAGCTCTCGGGGCTCCTCTGCTGCTGCCAGGTGCC 60
 DB 1 ATGGACATAGAGGCTCCCGCTCAGCTCTCGGGGCTCCTCTGCTGCTGCCAGGTGCC 60
 QY 61 AGATGTGACATCCAGATGACCCAGCTCTCCCTGTCTGACATCTGTAGGGGACAGA 120
 DB 61 AGATGTGACATCCAGATGACCCAGCTCTCCCTGTCTGACATCTGTAGGGGACAGA 120
 QY 121 GTACACATCACTTGGCAGGCAAGTGCAGCATTAAGTATTAATGGTATTCAGCAG 180
 DB 121 GTACACATCACTTGGCAGGCAAGTGCAGCATTAAGTATTAATGGTATTCAGCAG 180
 QY 181 AAACGAGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240
 DB 181 AAACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240
 QY 241 CCATCAAGTTTACGCGCAGTGTGATCTGGACAGAGTTCACTCTACCGTCAGCAGCTG 300
 DB 241 CCATCAAGTTTACGCGCAGTGTGATCTGGACAGAGTTCACTCTACCGTCAGCAGCTG 300
 QY 301 CAGCTGAGATTTTGGCACTATTACTGTCTACAGGTTTATAGTACCCTGGAGAGTTC 360
 DB 301 CAGCTGAGATTTTGGCACTATTACTGTCTACAGGTTTATAGTACCCTGGAGAGTTC 360
 QY 361 GGCCAGGAGCAAGGTGAAATCAAA 387
 DB 361 GGCCCGGAGCAAACTGATATCAAA 387

Db 361 GGCCAAGGACCAAGGTGGAATCAAA 387

RESULT 5

HUMIGKAN 406 bp mRNA linear PRI 28-OCT-1994

LOCUS Human rearranged Igk mRNA VJC region.

DEFINITION M87478

ACCESSION M87478

KEYWORDS C-region: 1 GI:185950

SOURCE C-region: V-region: immunoglobulin kappa-chain: immunoglobulin light chain.

ORGANISM Homo sapiens (individual isolate patient CHEB) bone marrow CDNA to mRNA.

REFERENCE Homo sapiens

AUCUTTER, P., BAUWENS, M., KHAMLICH, A. A., DEMOY, L., SPlneil, S., TOUCHARD, G., PREUD'homme, J. L. and COGNE, M. Monoclonal Ig L chain and L chain V domain fragment crystallization in myeloma-associated Fanconi's syndrome

JOURNAL J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)

MEDLINE 93224763

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/isolate="patient CHEB"

/db_xref="taxon:9606"

/map="2p12"

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/tissue_type="bone marrow"

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/gene="Igk"

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/protein_id="AA51019.1"

/db_xref="GI:185951"

/translation="MDMRVPAOLGLLLMLRGARCDIQMTOSPSLSASVGDRTFT

CRASOTIAFLNMYOQKPGKAPKLITYGASSIOSGVPSRSGSGSDTDTLTISLQPE

EDPATYCOQSYSTPRFTGGTVEIKRIRAR"

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/product="immunoglobulin kappa chain"

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/gene="Igk"

/note="VJ-J1 region"

389..>406

/gene="Igk"

<389..>406

/gene="Igk"

/note="this CDS feature is included to show the translation of the corresponding C-region. Presently translation qualifiers on C-region features are illegal."

/codon_start=1

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/db_xref="GI:561655"

/translation="RTVAP"

BASE COUNT 97 a 113 c 102 g 94 t

ORIGIN

Query Match 85.9%; Score 332.6; DB 9; Length 406; Pred. No. 3.8e-98;

Best Local Similarity 91.2%; Mismatches 34; Indels 0; Gaps 0;

Matches 353; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

1 ATGACATGAGGAGTCCCGCTCAGCTCCTGCGGCTCTTCTGCTGAGCCAGGAGTGC 60

2 ATGACATGAGGAGTCCCGCTCAGCTCCTGCGGCTCTTCTGCTGAGCCAGGAGTGC 61

Qy 61 AGATGTACATCCAGATGAGCCAGTCTCCATCTCCCTGTCGATCTGTAGGGACAGA 120

Db 62 AGATGTACATCCAGATGAGCCAGTCTCCATCTCCCTGTCGATCTGTAGGGACAGA 121

Qy 121 GTACCATCAGTCTGAGGAGCACTGACGACATTAAGTATATTAATGTGTCAGCAG 180

Db 122 GTACCATCAGTCTGAGGAGCACTGACGACATTAAGTATATTAATGTGTCAGCAG 181

Qy 181 AATCCAGAAAGCTCCTTACGCTCGATCTGATGTCATCCAGTTCGAAAGTGGGGTC 240

Db 182 AATCCAGAAAGCTCCTTACGCTCGATCTGATGTCATCCAGTTCGAAAGTGGGGTC 241

Qy 241 CCATCAAGGTTGACGCGAGTGTGATCTGGACAGAGTTCACTTCACGTCAGCAGCTG 300

Db 242 CCATCAAGGTTGACGCGAGTGTGATCTGGACAGAGTTCACTTCACGTCAGCAGCTG 301

Qy 301 CAGCTGAAAGATTTTGCAGTTATTTACTGCTACAGTTATAGTACCCCTGGAGCTTC 360

Db 302 CAACCTGAAGATTTTCACTTACTGCTACAGTTATAGTACCCCTGGAGCTTC 361

Qy 361 GGCCAAGGACCAAGGTGGAATCAAA 387

Db 362 GGCCAAGGACCAAGGTGGAATCAAA 388

RESULT 6

AF228327 400 bp DNA linear PRI 20-JUL-2000

LOCUS Homo sapiens clone BUS immunoglobulin light chain variable region

DEFINITION gene, partial cds.

ACCESSION AF228327

VERSION AF228327.1 GI:9295292

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 400)

AUTHORS Maloum, K., Dighiero, G. and Magnac, C. C.

TITLE Unmutated Ig VH genes in CLL patients

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 400)

AUTHORS Maloum, K., Dighiero, G. and Magnac, C. C.

TITLE Direct Submission

JOURNAL Submitted (13-JAN-2000) Physiopathology, Institut Pasteur, 28 rue du Dr Roux, Paris 75015, France

FEATURES

Location/Qualifiers

1..400

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="14"

/map="14q32-q39"

/clone="BUS"

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/note="Isolated from B-cell chronic lymphocytic leukemia patient"

<1..>400

/product="immunoglobulin light chain variable region"

<1..>400

/note="unmutated"

/codon_start=1

/product="immunoglobulin light chain variable region"

/protein_id="AA86916.1"

/db_xref="GI:9295293"

/translation="DMRVPAOLGLLLMLRGARCDIQMTOSPSLSASVGDRTFTC

RASOSISYINMYOQKPGKAPKLITYGASSIOSGVPSRSGSGSDTDTLTISLQPE

DPATYCOQSYSTPRFTGGTVEIKRIRAR"

BASE COUNT 99 a 109 c 100 g 92 t

ORIGIN

Query Match 85.6%; Score 331.2; DB 9; Length 400; Pred. No. 1.1e-97;

Best Local Similarity 91.4%;

Matches 351; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 GACATGAGGATCCCGCTCAGCTCTGAGGAGCTCTCTGCTGAGCTCCAGGTGCGAGA 63
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 Db 1 GACATGAGGATCCCGCTCAGCTCTGAGGAGCTCTCTGCTGAGCTCCAGGTGCGAGA 60
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QY 64 TGTGACATCCAGATGACCAAGTCTCATCTTCCCTGTCTGATCTGAGGAGACAGATC 123
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 Db 61 TGTGACATCCAGATGACCAAGTCTCATCTTCCCTGTCTGATCTGAGGAGACAGATC 120
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QY 124 ACCATGACTTGGAGGAGTACGACATTAGTATTATTAATTGATTCAGCAGAAA 183
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 Db 121 ACCATGACTTGGAGGAGTACGACATTAGTATTATTAATTGATTCAGCAGAAA 180
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QY 184 CCAGGAAAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAAAGTGGGTCGCCA 243
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 Db 181 CCAGGAAAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAAAGTGGGTCGCCA 240
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QY 244 TCAAGTTTCAAGCGGAGTGTGATCTGGAGACAGATTCATCTCAGCGTACAGCTGACAG 303
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 Db 241 TCAAGTTTCAAGCGGAGTGTGATCTGGAGACAGATTCATCTCAGCGTACAGCTGACAG 300
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QY 304 CCGAAGATTTTCCGATCTTACTGCTCTACAGTTTATGATCCCTCGAGCTGCGC 363
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 Db 301 CCGAAGATTTTCCGATCTTACTGCTCTACAGTTTATGATCCCTCGAGCTGCGC 360
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QY 364 CAAGGACCAAGGTGGAATCAAA 387
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 Db 361 CAAGGACCAAGGTGGAATCAAA 384
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RESULT 7
 HUMIGKVC 432 bp mRNA linear PRI 05-MAY-2000
 LOCUS Homo sapiens Immunoglobulin kappa light chain VC region (IGK) mRNA,
 DEFINITION partial cds.
 ACCESSION L013279
 VERSION L01279.1 GI:185984
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 432)
 Friedmann, D.F., Moore, J.S., Erikson, J., Manz, J., Goldman, J.,
 Nowell, P.C. and Silberstein, L.E.
 TITLE Variable region gene analysis of an isotype-switched (IgA) variant
 of chronic lymphocytic leukemia
 JOURNAL Blood 80 (9), 2287-2297 (1992)
 MEDLINE 93043344
 PUBMED 1421400
 FEATURES
 source Location/Qualifiers
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 CASQSISSYLMWYQOKPKARKLILYASSISLQSGVPSFGSGSTDTDTLLISSLP
 EEPATYYCOQSTSTPPWTFGCTKVEIKRTVAAPSVFIPTPS"
 sig_peptide 1..66

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 67..354
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BASE COUNT 103 a 126 c 102 g 101 t
 ORIGIN

Query Match 85.5%; Score 330.8; DB 9; Length 432;
 Best Local Similarity 92.3%; Pred. No. 1.5e-97;
 Matches 360; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

QY 1 ATGACATGAGGATCCCGCTCAGCTCTGAGGAGCTCTCTGCTGAGCTCCAGGTGCGC 60
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QY 61 AGATGTGACATCCAGATGACCAAGTCTCATCTTCCCTGTCTGATCTGAGGAGACAG 120
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QY 121 GTACCATCATCTTGGAGGAGTACGACATGATAGTATTATTAATTGATTCAGCAG 180
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 Db 121 GTACCATCATCTTGGAGGAGTACGACATGATAGTATTATTAATTGATTCAGCAG 180
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QY 181 AAACGAGAAAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAAAGTGGGTC 240
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 Db 181 AAACGAGAAAAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAAAGTGGGTC 240
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QY 241 CCATCAAGTTTCAAGCGGAGTGTGATCTGGAGACAGATTCATCTCAGCGTACAGCTG 300
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 Db 241 CCATCAAGTTTCAAGCGGAGTGTGATCTGGAGACAGATTCATCTCAGCGTACAGCTG 300
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QY 301 CACCTGAAGATTTTGGAGTCTTACTGCTCTACAGTTTATGATCCCTC--GGAGC 357
 |||||
 Db 301 CACCTGAAGATTTTGGAGTCTTACTGCTCTACAGTTTATGATCCCTC--GGAGC 350
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QY 358 TTGCGCCAAAGGACCAAGGTGGAATCAAA 387
 |||||
 Db 361 TTGCGCCAAAGGACCAAGGTGGAATCAAA 390
 |||||

RESULT 8
 MMU57579 390 bp mRNA linear PRI 02-OCT-1996
 LOCUS Macaca mulatta Ig rearranged light chain variable region, anti-RBC
 DEFINITION Macaca mulatta Ig rearranged light chain variable region, anti-RBC
 accession 057579
 ACCESSION U57579
 VERSION U57579.1 GI:1575105
 KEYWORDS
 SOURCE rhesus monkey.
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 REFERENCE 1 (bases 1 to 390)
 Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
 and Capra, J.D.
 TITLE Variable Region Gene Segment Utilization in Rhesus Monkey
 Hybridomas Producing Human Red Blood Cell-Specific Antibodies:
 Predominance of the VH4 Family but not VH4-21 (V4-34)
 JOURNAL Unpublished
 2 (bases 1 to 390)
 REFERENCES
 Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
 and Capra, J.D.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
 University of Texas Southwestern Medical Center, 6000 Harry Hines
 Blvd., Dallas, TX 75235-9140, USA
 FEATURES
 source Location/Qualifiers
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CDS
/organism="Macaca mulatta"
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/note="hybridoma 167"
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/codon_start=1
/product="immunoglobulin light chain"
/protein_id="AB09456.1"
/db_xref="GI:1575106"
/translation="MDMRAPAOILGLLLMLPCARCDIOMTQSPSSLSASVGDRTVT
CRASENVNLIHWYOOKPGKAPKILTYGSTLQSGVPSNFSGSGSDTDLTLLTSSLP
EDVATYYCOHSYSGTPTLFGGCTKVEIKR"

BASE COUNT 94 a 110 c 98 g 88 t
ORIGIN

Query Match 85.1%; Score 329.4; DB 9; Length 390;
Best Local Similarity 90.7%; Pred. No. 4.3e-97;
Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTCGGGCTCCTTGTGCTGCTGCCAGGTGCC 60
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QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATGTAGGGAGAGA 120
DB 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATGTAGGGAGAGA 120
QY 121 GTACACATCACTTGACAGGCAAGTCAAGCATTAAGTATTAAATTGATACAGAG 180
DB 121 GTACACATCACTTGACAGGCAAGTCAAGCATTAAGTATTAAATTGATACAGAG 180
QY 181 AAMCCAGAAAAGCTCTTAAGTCTCTGATCTATGTTCATTCAGTTGCAAAAGTGGGTC 240
DB 181 AAMCCAGAAAAGCTCTTAAGTCTCTGATCTATGTTCATTCAGTTGCAAAAGTGGGTC 240
QY 241 CCATCAAGGTTACAGCGGCAATGATGTGGAGAGTTCACTCTCACCCTGACAGCCTG 300
DB 241 CCATCAAGGTTACAGCGGCAATGATGTGGAGAGTTCACTCTCACCCTGACAGCCTG 300
QY 301 CAGCCTGAAGATTTTGGCACTTATTAAGTCTGACAGGTTATAGTACCCCTCGAGCCTTC 360
DB 301 CAGCCTGAAGATTTTGGCACTTATTAAGTCTGACAGGTTATAGTACCCCTCGAGCCTTC 360
QY 361 GCCCAAGGACCAAGGTGGAATCAAA 387
DB 361 GCCCAAGGACCAAGGTGGAATCAAA 387

RESULT 9

AX305000 AX305000 974 bp DNA linear PAT 11-DEC-2001
LOCUS
DEFINITION Sequence 29 from Patent EP1158004.
ACCESSION AX305000
VERSION AX305000.1 GI:117644678
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL 1 (sites)
Takashit, T., Katsunari, T. P. and Nobuaki, H.
Human monoclonal antibody against a costimulatory signal
transduction molecule a11m and pharmaceutical use thereof
Patent: EP 1158004-A 29 28-NOV-2001;
Japan Tobacco Inc. (JP)

FEATURES
source Location/Qualifiers
1..974
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/db_xref="taxon:9606"
1..38
39..749
/note="unnamed protein product"
/codon_start=1

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/translation="MDMRAPAOILGLLLMLPGRSARDIOMTQSPSSLSASVGDRTVT
CRASQISRLIAHWYOOKPGKAPKILTYVASLSQSGVPSNFSGSGSDTDLTLLTSSLP
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EYPRKVKQWIKVNDNALQSGNSQSEVTEDSKDYSLSTLLSLKADYERKHYACEV
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39..104
750..974
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ORIGIN

Query Match 85.1%; Score 329.4; DB 6; Length 974;
Best Local Similarity 90.7%; Pred. No. 4.5e-97;
Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTCGGGCTCCTTGTGCTGCTGCCAGGTGCC 60
DB 39 ATGGACATGAGGGTCCCGCTCAGCTCTCGGGCTCCTTGTGCTGCTGCCAGGTGCC 98
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATGTAGGGAGAGA 120
DB 99 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATGTAGGGAGAGA 158
QY 121 GTACACATCACTTGACAGGCAAGTCAAGCATTAAGTATTAAATTGATACAGAG 180
DB 159 GTACACATCACTTGACAGGCAAGTCAAGCATTAAGTATTAAATTGATACAGAG 218
QY 181 AAMCCAGAAAAGCTCTTAAGTCTCTGATCTATGTTCATTCAGTTGCAAAAGTGGGTC 240
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QY 241 CCATCAAGGTTACAGCGGCAATGATGTGGAGAGTTCACTCTCACCCTGACAGCCTG 300
DB 279 CCATCAAGGTTACAGCGGCAATGATGTGGAGAGTTCACTCTCACCCTGACAGCCTG 338
QY 301 CAGCCTGAAGATTTTGGCACTTATTAAGTCTGACAGGTTATAGTACCCCTCGAGCCTTC 360
DB 339 CAGCCTGAAGATTTTGGCACTTATTAAGTCTGACAGGTTATAGTACCCCTCGAGCCTTC 398
QY 361 GCCCAAGGACCAAGGTGGAATCAAA 387
DB 399 GCCCAAGGACCAAGGTGGAATCAAA 425

RESULT 10

AX306529 AX306529 974 bp DNA linear PAT 11-DEC-2001
LOCUS
DEFINITION Sequence 29 from Patent WO0187981.
ACCESSION AX306529
VERSION AX306529.1 GI:17645749
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL 1 (sites)
Tsuiji, T., Tezuka, K. and Horii, N.
Human monoclonal antibody against a costimulatory signal
transduction molecule a11m and pharmaceutical use thereof
Patent: WO 0187981-A 29 22-NOV-2001;
Japan Tobacco Inc. (JP)

FEATURES
source Location/Qualifiers
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1..38
39..749
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/codon_start=1
/protein_id="CAD19048.1"
/db_xref="GI:17645750"

JOURNAL Submitted (03-NOV-1993) M. Zouali, Institut Pasteur, Immunogenetique Cellulaire, 28 Rue du Dr. Roux, 75015 Paris, FRANCE
REFERENCE 3 (bases 1 to 396)
AUTHORS Bensimon,C., Chastagner,P. and Zouali,M.
TITLE Human lupus anti-DNA autoantibodies undergo essentially primary V kappa gene rearrangements
JOURNAL EMBO J. 13 (13), 2951-2962 (1994)
MEDLINE 94131975
FEATURES
source Location/Qualifiers
1..396
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/db_xref="taxon:9606"
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/cell_type="PBL"
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V_region
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73..357
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358..396
/note="JK1"
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Best Local Similarity 90.2%; Pred. No. 4.6e-96;
Matches 343; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGACATGAGAGGTCCTCCGCTCAGCTCCTGCGGCTCCTTGTGCTGCTGCCAGGTGCC 60
Db 7 ATGACATGAGAGGTCCTCCGCTCAGCTCCTGCGGCTCCTTGTGCTGCTGCCAGGTGCC 66
QY 61 AGATGTGACATCCAGATGAGCCAGTCTCCATCTTCCCTGCTGATCTGAGGAGACAGA 120
Db 67 AGATGTGACATCCAGATGAGCCAGTCTCCATCTTCCCTGCTGATCTGAGGAGACAGA 126
QY 121 GTCAACATCCTTCAGAGGCAAGTCAGACATAGTATTATTTAAATTTGATACAGAG 180
Db 127 GTCAACATCCTTCAGAGGCAAGTCAGACATAGTATTATTTAAATTTGATACAGAG 186
QY 181 AACCAGGAAAGCTCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240
Db 187 AACCAGGAAAGCTCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 246
QY 241 CCATCAAGGTTCAAGGCGAGTGTGAGACAGAGTTCACCTCAGCAGAGCCTG 300
Db 247 CCATCAAGGTTCAAGGCGAGTGTGAGACAGAGTTCACCTCAGCAGAGCCTG 306
QY 301 CAGCCTAAGATTTGGAGCTTACTGTCTACAGGTTATATACCCCTCGACGTTTC 360
Db 307 CAGCCTAAGATTTGGAGCTTACTGTCTACAGGTTATATATACCCCTCGACGTTTC 366
QY 361 GGCCAGGAGCAAGTGTGAATCAA 387
Db 367 GGCCAGGAGCAAGTGTGAATCAA 393
RESULT 13
LOCUS HSIGKLV56 383 bp mRNA linear PRI 31-JAN-1994
DEFINITION H.sapiens mRNA for rearranged Ig kappa light chain variable region (1.23).
ACCESSION X72477.1 GI:441422
VERSION X72477.1
KEYWORDS C-region; Immunoglobulin; J-segment; kappa light chain; V-region.
SOURCE human.

ORGANISM Homo sapiens
REFERENCE 2 (bases 1 to 383)
AUTHORS Klein,R., Jeenichen,R. and Zachau,H.G.
TITLE Expressed human immunoglobulin kappa genes and their hypermutation
JOURNAL Eur. J. Immunol. 23 (12), 3248-3262 (1993)
MEDLINE 94080891
FEATURES
source Location/Qualifiers
1..383
/organism="Homo sapiens"
/isolate="M.I."
/db_xref="taxon:9606"
/chromosome="2"
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1..383
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CDS
1..383
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V_segment
337..375
/note="J-kappa 1"
J_segment
376..383
C_region
96 a 107 c 93 g 87 t
BASE COUNT 96 a 107 c 93 g 87 t
ORIGIN
Query Match 84.1%; Score 325.6; DB 9; Length 383;
Best Local Similarity 92.2%; Pred. No. 7.6e-96;
Matches 343; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 16 CCCGCTCAGCTCTGGGGCTCCTTGTGCTGCGCTCCAGTGCAGATGACATCCAG 75
Db 1 CCCGCTCAGCTCTGGGGCTCCTTGTGCTGCGCTCCAGTGCAGATGACATCCAG 60
QY 76 ATGACCAAGTCTCCATCTTCCCTGCTGATCTGATCTGATCTGATCTGATCTGATCTG 135
Db 61 ATGACCAAGTCTCCATCTTCCCTGCTGATCTGATCTGATCTGATCTGATCTGATCTG 120
QY 136 AGGCAAGTCAAGCATTTAGTATTATTTAAATTTGATACAGCAAGCAAGCAAGCAAGCT 195
Db 121 CGGCAAGTCAAGCATTTAGTATTATTTAAATTTGATACAGCAAGCAAGCAAGCAAGCT 180
QY 196 CCTAAGCTCCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 255
Db 181 CCTAAGCTCCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240
QY 256 GGCAGTGAATCTGGAGAGATTCACCTCAGCAGAGCTGCAAGCTGAAGATTTC 315
Db 241 GGCAGTGAATCTGGAGAGATTCACCTCAGCAGAGCTGCAAGCTGAAGATTTC 300
QY 316 GCGACTTATTACTGTCTACAGGTTTATAGTACCCCTGGACGTTCCGCAAGGACCAAG 375
Db 301 GCAACTTACTACTGTCAACAGAGTTACATACCCCGTGGAGCTTCGCGCAAGGACCAAG 360
QY 376 GTGGAATCAA 387
Db 361 GTGGAATCAA 372

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	JOURNAL	MEDLINE	FEATURES
HSIGKLV06	H.sapiens mRNA for rearranged Ig kappa light chain variable region (1.45).	X72427.1	GI:441322	immunoglobulin; J-segment; kappa light chain; V-region.	human	Homo sapiens	Submitted (25-APR-1993)	H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2, FRG			
LOCUS	HSIGKLV06	389 bp	mRNA	linear	PRI 31-JAN-1994						
DEFINITION	H.sapiens mRNA for rearranged Ig kappa light chain variable region (1.45).										
ACCESSION	X72427.1	GI:441322									
VERSION	X72427										
KEYWORDS	immunoglobulin; J-segment; kappa light chain; V-region.										
SOURCE	human										
ORGANISM	Homo sapiens										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.										
AUTHORS	1 (bases 1 to 389)										
JOURNAL	Zachau, H.G.										
MEDLINE	Direct submission										
FEATURES	Submitted (25-APR-1993) H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2, FRG										
FEATURES	2 (bases 1 to 389)										
AUTHORS	Klein, R., Jaenichen, R. and Zachau, H.G.										
JOURNAL	Expressed human immunoglobulin kappa genes and their hypermutation										
MEDLINE	Eur. J. Immunol. 23 (12), 3248-3262 (1993)										
FEATURES	94080891										
SOURCE	Location/Qualifiers										
FEATURES	1..389										
AUTHORS	/organism="Homo sapiens"										
JOURNAL	/isolate="M.L."										
MEDLINE	/db_xref="taxon:9606"										
FEATURES	/chromosome="2"										
AUTHORS	/clone="I.45"										
JOURNAL	/tissue_type="spleen"										
MEDLINE	/clone_lib="lambda zap II phage library"										
FEATURES	1..389										
AUTHORS	/partial										
JOURNAL	/codon_start=3										
MEDLINE	/product="Ig kappa light chain (VJ)"										
FEATURES	/protein_id="CA51095.1"										
AUTHORS	/db_xref="GI:441323"										
JOURNAL	/translation="DMRVPADLLLLILWLGKAGCDIQMTPSSLSLSDRYVTTC										
MEDLINE	RASQISIGTYLWYQKPKAKPLIYGASLSQSGVPSRFSGSGSDFTFLTISLSLOPE										
FEATURES	DFATYVCOQYTSFPTFGGKVEIKL"										
AUTHORS	1..389										
JOURNAL	/product="Ig kappa light chain (VJ)"										
MEDLINE	65..350										
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AUTHORS	/note="J-Kappa 4"										
JOURNAL	/base_count	94 a 109 c 94 g 92 t									
MEDLINE	ORIGIN										
FEATURES	BASE COUNT	94 a 109 c 94 g 92 t									
AUTHORS	Query Match	83.6%; Score 333.6; DB 9; Length 389;									
JOURNAL	Best Local Similarity	89.9%; Pred. No. 3.5e-95;									
MEDLINE	Matches 347; Conservative 0; Mismatches 39; Indels 0; G										

LOCUS	AX327729	728 bp	DNA	linear	PAT 07-JAN-2002
DEFINITION	Sequence 15 from Patent WO0183755.				
ACCESSION	AX327729				
VERSION	AX327729.1	GI:18098040			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (sites)				
AUTHORS	Mikayama,T., Takahashi,N., Chen,X. and Schoenberger,S.P.				
TITLE	Human anti-cd40 antibodies and methods of making and using same				
JOURNAL	Patent: WO 0183755-A 15 08-NOV-2001;				
	Gemini Science, Inc. (US)				
FEATURES	Location/Qualifiers				
source	1..728				
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	/db_xref="taxon:9606"				
BASE COUNT	183 a	201 c	195 g	149 t	
ORIGIN					

Query Match	83.5%	Score 323	DB 6	Length 728
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Matches 347	Conservative 0	Mismatches 40	Indels 0	Gaps 0
QY 1	ATGCACATGAGGGTCCCGCTCAGCTCCTCGGGGCTCCTTCGTGCTCTGCTCCAGGTCC	60		
Db 59	ATGCACATGAGGGTCCCGCTCAGCTCCTCGGGGCTCCTTCGTGCTCTGCTCCAGGTCC	118		
QY 61	AGATGTGACATTCAGATATACCCAGTCTCCATCTTCCCTGTCTGCAATCTGTAGGGACAGA	120		
Db 119	AGATGCGCATTCACATATACCCAGTCTCATCTCCGCTGTGATCTGTAGAGACAGA	178		
QY 121	GTACACATTCACCTTGAGGAGCAAGTAGACATATTAGTATTATTAAATGTGATCAGAG	180		
Db 179	GTACACATTCACCTTGCGGGCGAGTATAGGGATATTAGCAGCTGGTTAGCCTGGATATACGAG	238		
QY 181	AAACCGAGAAAAAGCTCTGTAAGCTCTGATCTATATGTTGATCCAGTTTGCAAAAGTGGGTC	240		
Db 239	AAACCGAGGAAAAAGCCCTTAAGCTCTGATCTGATCTGATCCAGTTTGCAAAAGTGGGTC	298		
QY 241	CCATCAAGGTTCAGGGGAGTGTGATCTGGGACAGAGTTCATCACTCAACGTCAGACGCTG	300		
Db 299	CCATCAAGGTTCAGGGGAGTGTGATTTGGACAGATTCCTCACTCAACATCAGCAGCTG	358		
QY 301	CAGCCTGAAGATTTTGGCACTATTATTCGTCTTACAGAGTTTATAGTACCCTCGAGCTTC	360		
Db 359	CAGCCTGAAGATTTTGGCAACTATTACTATTGTCTCAACAGGCTAGTATTTCCCTCGGACATTC	418		
QY 361	GGCCCAAGGAGCCCAAGGTGGAATCAAA	387		
Db 419	GGCCCAAGGAGCCCAAGGTGAGATCAAA	445		

Search completed: September 23, 2002, 17:50:12
 Job time: 6866 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:06:51 ; Search time 3874.81 Seconds

(without alignments)
1348.020 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGGACATGAGGTCGCCG.....GGACCAAGTGGAATCATA 387

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbta:*
2: em_estbhm:*
3: em_estin:*
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5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343.4	88.7	493	9	AM405753 UT-HF-BL0
2	332.6	85.9	891	10	BG540787 602570674
3	329.6	85.2	724	10	BG537031 602565115
4	329.4	85.1	867	10	BG754732 602714301
5	329.4	85.1	886	10	BG756818 602710291
6	327.8	84.7	864	10	BG548281 602575248
7	326.6	84.4	391	9	AM404992 UT-HF-BL0
8	326.2	84.3	453	9	AM383563 PM4-HM034
9	324.6	83.9	447	9	AM405752 UT-HF-BL0
10	321.6	83.1	669	10	BG541198 602569978
11	321.4	83.0	770	10	BG689444 602637305
12	321.4	83.0	943	10	BF976230 602245105
13	321.4	83.0	1100	10	BF663472 602144635
14	320.6	82.8	712	10	BG538665 602566902
15	320.6	82.8	921	10	BG341239 602463904
16	319	82.4	557	10	BG760164 602733253
17	319	82.4	1038	10	BG757218 602710591

18	318.8	82.4	655	10	BG569796 602590416
19	318.8	82.4	858	10	BG756326 602713645
20	318.2	82.2	867	10	BG539961 602567476
21	318.2	82.2	867	10	BG535392 602563053
22	317.6	82.1	437	9	AM404458 UT-HF-BL0
23	317.4	82.0	817	10	BG432453 602495486
24	317.2	82.0	471	9	AM406294 UT-HF-BL0
25	317	81.9	566	9	AM406081 UT-HF-BL0
26	316.8	81.9	420	9	AV683828 AV683828
27	316.8	81.9	927	10	BG536845 602566383
28	316.6	81.8	755	10	BG533970 602553071
29	316.6	81.8	921	10	BG758398 602712592
30	316.4	81.7	431	9	AM406886 UT-HF-BL0
31	315.6	81.6	472	9	AM406323 UT-HF-BL0
32	315	81.4	680	9	AV733319 AV733319
33	315	81.4	711	10	BG546866 602574048
34	315	81.4	920	10	BG740562 602563076
35	314	81.1	813	10	BG431143 602498773
36	313.4	81.0	487	9	AM405988 UT-HF-BL0
37	313	80.9	714	10	BG757897 602714929
38	313	80.9	750	10	BG755394 602713951
39	311.8	80.6	721	10	BG686441 602638377
40	311.8	80.6	727	10	BG684242 602635874
41	311.8	80.6	744	10	BT61857 603048792
42	311.4	80.5	706	10	BG759950 602733557
43	311.4	80.5	1130	10	BF662874 602144820
44	311	80.4	688	10	BG539229 602567825
45	311	80.4	851	10	BG686018 602638582

ALIGNMENTS

RESULT 1
LOCUS AM405753 493 bp mRNA linear EST 16-FEB-2000
DEFINITION UT-HF-BL0-abp-a-02-0-UT-RI NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057290 5', mRNA sequence.
ACCESSION AM405753
VERSION AM405753.1 GI:6924810
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC <http://mgi.ncl.nih.gov/>
1 (bases 1 to 493)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbp/image/image.html
Seq primer: M3 Forward.

FEATURES

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/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/note="Vector: pT7n3-Pac; Site1: NotI; Site2: Eco RI; constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

SOURCE ORGANISM	human.
	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 886)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLCMI692 row: e column: 23
High quality sequence stop: 864.
Location/Qualifiers
1. 886
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:485086"
/clone_1lb="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 211 a 258 c 219 g 197 t 1 others
ORIGIN
Query Match 85.1%; Score 329.4; DB 10; Length 886;
Best Local Similarity 90.7%; Pred. No. 1.2e-89;
Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGTGCC 60
DB 10 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGTGCC 69
QY 61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCCTGTCTGCATCTGAGGAGACA 120
DB 70 AGGTGTGACATCCAGATGACCCAGTCTCATCTTCCCTGTCTGCATCTGAGGAGACA 129
QY 121 GTACCATCTTGCAGGGGCAAGTCAAGATTAAGTATTAAATTGGTATCAGAG 180
DB 130 GTACCATCTTGCAGGGGCAAGTCAAGATTAAGTATTAAATTGGTATCAGAG 189
QY 181 AAACCAAGAAAGCTCTTAAGTCTCGATATATGTTGATCCAGTTGCAAGGGGGTC 240
DB 190 AAACCAAGAAAGCTCTTAAGTCTCGATATATGCTGATCCAGTTGCAAGGGGGTC 249
QY 241 CCATCAAGGTTTCAGCGGAGTGTGAGTGGACAGAGTTCACTCTCAACCTCAGCAGCTG 300
DB 250 CCATCAAGGTTTCAGCGGAGTGTGAGTGGACAGAGTTCACTCTCAACATCAGCAGCTG 309
QY 301 CAGCTGAAAGATTTTGCAGTATTAAGTGTCTAAGGTTTATAGTACCCCTCGAGCTTC 360
DB 310 CAGCTGAAAGATTTTGCAGTATTAAGTGTCTAAGGTTTATAGTACCCCTCGAGCTTC 369
QY 361 GGGCAAGGAGCAAGGTGGAATCAAA 387
DB 370 GGGCTGGGGACCAAGCTGGAGATCAAA 396
RESULT 6
BG548281

LOCUS BG548281 864 bp mRNA linear EST 04-APR-2001
DEFINITION 602575248F1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4703483 5',
mRNA sequence.
ACCESSION BG548281
VERSION BG548281.1 GI:13546946
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 864)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Clontech Laboratories, Inc.
CDNA Library Preparation: Clontech Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLCMI541 row: p column: 12
High quality sequence stop: 726.
Location/Qualifiers
1. 864
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4703483"
/clone_1lb="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGGCAATATGAGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCGGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
BASE COUNT 215 a 253 c 209 g 187 t
ORIGIN
Query Match 84.7%; Score 327.8; DB 10; Length 864;
Best Local Similarity 90.4%; Pred. No. 3.6e-89;
Matches 350; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGTGCC 60
DB 27 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGTGCC 86
QY 61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCCTGTCTGCATCTGAGGAGACA 120
DB 87 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCCTGTCTGCATCTGAGGAGACA 146
QY 121 GTACCATCTTGCAGGGGCAAGTCAAGATTAAGTATTAAATTGGTATCAGAG 180
DB 147 GTACCATCTTGCAGGGGCAAGTCAAGATTAAGTATTAAATTGGTATCAGAG 206
QY 181 AAACCAAGAAAGCTCTTAAGTCTCGATATATGTTGATCCAGTTGCAAGGGGGTC 240
DB 207 AAACCAAGAAAGCTCTTAAGTCTCGATATATGCTGATCCAGTTGCAAGGGGGTC 266
QY 241 CCATCAAGGTTTCAGCGGAGTGTGAGTGGACAGAGTTCACTCTCAACCTCAGCAGCTG 300
DB 267 CCATCAAGGTTTCAGCGGAGTGTGAGTGGACAGAGTTTCACTCTCAACATCAGCAGCTG 326
QY 301 CAGCTGAAAGATTTTGCAGTATTAAGTGTCTAAGGTTTATAGTACCCCTCGAGCTTC 360
DB 327 CAACCTGAAAGATTTTGCAGTATTAAGTGTCTAAGGTTTATAGTACCCCTCGAGCTTC 386

QY 361 GGCCAAAGGACCAAGTGGAATCAAA 387
 DB 387 GGGGAGGAGCACACGGGTGAGATCAAA 413
 RESULT 7
 AM404992 391 bp mRNA linear EST 16-FEB-2000
 LOCUS UI-HF-BL0-abx-a-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 DEFINITION IMAGE:3058060 5', mRNA sequence.
 AM404992
 ACCESSION AM404992.1 GI:6924049
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 391)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers
 1..391
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1img=3058060"
 /clone_1lib="NIH_MGC_37"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LT1)"
 /note="Vector: p7713-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 98 a 108 c 94 g 91 t
 ORIGIN
 Query Match 84.4%; Score 326.6; DB 9; Length 391;
 Best Local Similarity 91.1%; Pred. No. 5.9e-89;
 Matches 347; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 7 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGCTCCAGTCCAGATGT 66
 DB 5 AGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGCTCCAGTCCAGATGT 64
 QY 67 GACATCCAAATGACCAAGTCTCCCTGTCTGATCTTAGGGGACAGATCACC 126
 DB 65 GACATCCAAATGACCAAGTCTCCCTGTCTGATCTTAGGGGACAGATCACC 124
 QY 127 ATCACTTGACGGCAAGTCCAGATTAAGTATTAATGATGATCAGCAAAACA 186
 DB 125 ATCACTTGACGGCAAGTCCAGATTAAGTATTAATGATGATCAGCAAAACA 184
 QY 187 GGAAGAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTCCCATCA 246
 DB 185 GGAAGAGCTCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTCCCATCA 244
 QY 247 AGGTTACGGGGCAGTGGATCTGGGACAGAGTCTACCTCAGCGTCCAGACCTGACGCT 306

DB 245 AGGTTACGGGGCAGTGGATCTGGGACAGATTTCACTTCCATCAGACATCTACCACT 304
 QY 307 GAAGATTTTGCAGCTATTATCTCTACAGGTTATAGTACCCCTGGAGCTCGGCCAA 366
 DB 305 GAAGATTTTGCAGCTATTATCTCTACAGGTTATAGTACCCCTGGAGCTCGGCCAA 364
 QY 367 GGGACCAAGGTGGAATCAAA 387
 DB 365 GGGACCAAGGTGGAATCAAA 385

RESULT 8
 AM383563 453 bp mRNA linear EST 04-FEB-2000
 LOCUS PM4-HT0348-261199-001-A07 HT0348 Homo sapiens cDNA, mRNA sequence.
 DEFINITION AM383563
 ACCESSION AM383563.1 GI:6888131
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 453)
 HCGP http://www.ludwig.org.br/ORESTES.
 AUTHORS The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL:
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM4&t2=PM4-HT0348-
 261199-001-A07&t3=1999-11-26&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 452.
 Location/Qualifiers
 1..453
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lib="HT0348"
 /dev_stage="Adult"
 /note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 tissues into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 108 a 125 c 107 g 113 t
 ORIGIN
 Query Match 84.3%; Score 326.2; DB 9; Length 453;
 Best Local Similarity 90.2%; Pred. No. 8.3e-89;
 Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGCTCCAGTCCAGTCC 60
 DB 5 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTCTGCTGCTCCAGTCCAGTCC 64
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCTGATCTGATGAGGACAGA 120
 DB 65 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCTGATCTGATGAGGACAGA 124
 QY 121 GTCACATCCTTGGAGGGCAGTCCAGATTAAGTATTAATGATGATCAGCAG 180
 DB 125 GTTACATCCTTGGAGGGCAGTCCAGATTAAGTATTAATGATGATCAGCAG 184

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QY 181 AACACAGAAAGCTCTTAAGTCTGATCTATGTGATCCATTCAGATTGCAAGTGGGTC 240
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Db 185 AAACAGAGAAAGCCCTCAGTTCCTATCTATCTGATCTGATTTGCAAGTGGGTC 244
QY 241 CCATCAAGTTTCAGCGGAGTGTGAGACAGAGTTCACTCTCACCGTCAGAGCCTG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 245 CCAACACAGTTTCAGTGTGATCTGAGACAGACTTCACTCTCACCATCAGAGTCTG 304
QY 301 CAGCTGAAGATTTGGAGCTTATCTACTGCTACAGTTTATAGTACCCTCGAGCTTC 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 305 CAACCTGAAGATTTGGAGCTTATCTACTGTCAACAGACTTATACCTCCCTGAGAGTTC 364
QY 361 GGGCAAGGAGCAAGGTGAAATCAAA 387
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 365 GGCCAAGGAGCAAGGTGAAATCAAA 391

RESULT 9
AM405752 447 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BL0-a-01-0-UI.r1.NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057288 5', mRNA sequence.
ACCESSION AM405752
VERSION AM405752.1 GI:6924809
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.dlo.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
FEATURES
source
1. 447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3057288"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germlinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/notes="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldto, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 105 a 129 c 111 g 102 t
ORIGIN
Query Match 83.9%; Score 324.6; DB 9; Length 447;
Best local similarity 89.9%; Pred. No. 2.5e-88;
Matches 348; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTGGGCTCTTCTGCTGCTCCAGGTGCC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 17 ATGACATGAGGGTCCCGCTCAGCTCTGGGCTCTTCTGCTGCTCCAGGTGCC 76
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AGATGTGACATCCAGATGACCCAGTCTTCATCTTCCCTGCTGATCTGTAGGGGACAGA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 77 AGATGTGACATCCAGATGACCCAGTCTTCATCTCCCTGCTGATCTGTAGGAGACAGA 136
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QY 121 GTACCACTACCTTCAGGCAAGTACAGACATTAGATTATTTAAATTTGGTATCACAG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 137 GTCCACCATTCATCTCCGCGGCAAGTACAGACATTATTTAAATTTGGTATCACAG 196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 AAACAGAGAAAGCTCTTAAGTCTGATCTATGTGATCCATTCAGATTGCAAGTGGGTC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 197 AGACAGAGAAAGCCCTCAGTTCCTATCTATCTGATCTGATTTGCAAGTGGGTC 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 CCATCAAGTTTCAGCGGAGTGTGAGACAGAGTTCACTCTCACCGTCAGAGCCTG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 CCATCAAGTTTCAGTGTGATCTGAGACAGATTTCACCTCTCACCATCAGAGTCTG 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 CAGCTGAAGATTTGGAGCTTATCTACTGCTACAGTTTATAGTACCCTCGAGCTTC 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 CAACCTGAAGATTTGGAGCTTATCTACTGTCAACAGACTTATACCTCCCTGAGAGTTC 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 GGGCAAGGAGCAAGGTGAAATCAAA 387
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 GGCCAAGGAGCAAGGTGAAATCAAA 403

RESULT 10
BG541198 669 bp mRNA linear EST 03-APR-2001
LOCUS 60256597Bf1.NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694539 5',
DEFINITION mRNA sequence.
ACCESSION BG541198
VERSION BG541198.1 GI:13533431
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 669)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1518 row: k column: 20
High quality sequence stop: 658.
Location/Qualifiers
FEATURES
source
1. 669
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4694539"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgagctggcc); Site_2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTGAGAGCGCGAGCGGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 177 a 189 c 164 g 139 t
ORIGIN
Query Match 83.1%; Score 321.6; DB 10; Length 669;

```

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

BASE COUNT	197 a	229 c	185 g	158 t	1 others
ORIGIN					

Query Match 83.0%; Score 321.4; DB 10; Length 770;

Matches	346	Conservative	0	Mismatches	41	Indels	0	Gaps	0
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1. **История создания и развития**

4

[illegible]

121 GTCACCAATCACCTTGCAGGGGCAAGTCAGGACAATTAGGTAATTAAATTGGATCAGCAG

Db 127 GTCAACATCACTTGGCCGACAAAGTCAGAGAATTAGCAGCTATTCAATTGGTATCAGCAG 10

181 AAACCAGGAAAGCTCCTAAGTCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGCTC 24

187

9

THE UNIVERSITY OF CHICAGO

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

DD 30/ CAACCGAAGATTTTGCACCTTAC TAC TGTCAACAGAGT TACAT TACCCCTCCCACTTTC

QY 361 GCCCAAGGACCAAGGTGGAATCAA 387

Db 367 GGGCCCTGGGACCAAGTGTATCAAA 393

RESULT 12

LOCUS	BF976230	943 bp	mRNA	linear	EST 22-J
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MRNA sequence

ACCESSION BF 370230
 NUMBER PD076030 1 DT 1034344E

KEYWORDS

ORGANISM Homo sapiens

Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo

REFERENCE 1 (BASES 1 TO 343)

FILE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Louis M. Straudt, M.D., Ph.D.

CONA LIBRARY REPLICATION: LING HONG/KUBILI LABORATORY

DNA Sequencing by: Incyte Genomics, Inc.

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: TJCMI208 row: 1 column: 02

high quality sequence stop. /z/.
 Tactile (Qual): 61.9%

source	1. .943
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/db_xref="taxon:9606"
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14b¹¹ NTH MGT 48"

/tissue-type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACAG(C). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 238 a 265 c 241 g 199 t

ORIGIN

Query Match 83.0%; Score 321.4; DB 10; Length 943;
 Best Local Similarity 89.4%; Pred. No. 3.4e-87;
 Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 ATGACATGAGGTCGCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGTGCC 60
 |||
 DB 18 ATGACATGAGGTCGCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGTGCC 77

QY 61 AGATGTGACATCCAGATGATGACCATCTCCCTGCTGATCTGTAGGGACAGA 120
 |||
 DB 78 AGATGTGACATCCAGATGATGACCATCTCCCTGCTGATCTGTAGGGACAGA 137

QY 121 GTCACCATCTTGCAGGCGAAGTCAGGACATGATTAATTAATTTGGTATCAGAG 180
 |||
 DB 138 GTCACCATCTTGCAGGCGAAGTCAGGACATGATTAATTAATTTGGTATCAGAG 197

QY 181 AAACGAGAAAGCTCTTACCTCTGATCTATGTTGATCAGTTGGCAAGTGGGCTC 240
 |||
 DB 198 AAACGAGAAAGCTCTTACCTCTGATCTATGTTGATCAGTTGGCAAGTGGGCTC 257

QY 241 CCATCAAGGTTTCAGCGGACAGTGTGAGACAGAGTTCACTCTCAGCGTACAGCCTG 300
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 DB 258 CCATCAAGGTTTCAGCGGACAGTGTGAGACAGAGTTCACTCTCAGCGTACAGCCTG 317

QY 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCTTC 360
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 DB 318 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCTTC 377

QY 361 GGCCAGGAGCAAGGTGGAATCAAA 387
 |||
 DB 378 GGCCAGGAGCAAGGTGGAATCAAA 404

RESULT 13
 BF663472 1100 bp mRNA linear EST 21-DEC-2000
 LOCUS 602144635F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297736 5',
 mRNA sequence.
 VERSION BF663472
 KEYWORDS BF663472.1 GI:11937367
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1100)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Louis M. Straudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: L10M152 row: f column: 09
 High quality sequence stop: 704.
 Location/Qualifiers
 1 1100
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4297736"
 /clone_1db="NIH_MGC_48"
 /tissue-type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACAG(C). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 283 a 308 c 270 g 239 t

ORIGIN

Query Match 83.0%; Score 321.4; DB 10; Length 1100;
 Best Local Similarity 89.4%; Pred. No. 3.7e-87;
 Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 ATGACATGAGGTCGCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGTGCC 60
 |||
 DB 8 ATGACATGAGGTCGCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGTGCC 67

QY 61 AGATGTGACATCCAGATGATGACCATCTCCCTGCTGATCTGTAGGGACAGA 120
 |||
 DB 68 AGATGTGACATCCAGATGATGACCATCTCCCTGCTGATCTGTAGGGACAGA 127

QY 121 GTCACCATCTTGCAGGCGAAGTCAGGACATGATTAATTAATTTGGTATCAGAG 180
 |||
 DB 128 GTCACCATCTTGCAGGCGAAGTCAGGACATGATTAATTAATTTGGTATCAGAG 187

QY 181 AAACGAGAAAGCTCTTACCTCTGATCTATGTTGATCAGTTGGCAAGTGGGCTC 240
 |||
 DB 188 AAACGAGAAAGCTCTTACCTCTGATCTATGTTGATCAGTTGGCAAGTGGGCTC 247

QY 241 CCATCAAGGTTTCAGCGGACAGTGTGAGACAGAGTTCACTCTCAGCGTACAGCCTG 300
 |||
 DB 248 CCATCAAGGTTTCAGCGGACAGTGTGAGACAGAGTTCACTCTCAGCGTACAGCCTG 307

QY 301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCTTC 360
 |||
 DB 308 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCTTC 367

QY 361 GGCCAGGAGCAAGGTGGAATCAAA 387
 |||
 DB 368 GGCCAGGAGCAAGGTGGAATCAAA 394

RESULT 14
 BG538665 712 bp mRNA linear EST 03-APR-2001
 LOCUS 602566902F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691280 5',
 mRNA sequence.
 VERSION BG538665
 KEYWORDS BG538665.1 GI:13530898
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 712)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: CLOMTECH Laboratories, Inc.
 cDNA Library Preparation: CLOMTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LILCM1510 row: d column: 01
 High quality sequence stop: 664.
 Location/Qualifiers

FEATURES

source

1. 712
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4691280"
 /clone_lib="NIH_MGC_77"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site: 1; flifi (ggcgccctggcc); Site: 2: flifi (ggcgccatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCCGACATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT

175 a 209 c 177 g 151 t

ORIGIN

Query Match 82.8%; Score 320.6; DB 10; Length 712;
 Best Local Similarity 91.0%; Pred. No. 5.3e-87;
 Matches 352; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

1 ATGACATGAGGAGTCCCGCTCAGCTCCTGCGGCTCCTGCTGCTGCGGCTCCAGAGTGC 60
 27 ATGACATGAGGAGTCCCGCTCAGCTCCTGCGGCTCCTGCTGCTGCGGCTCCAGAGTGC 86
 61 AGATGTGACATCCAGATGACCCAGATCTCATCTTCCCTGCTGCTGCTGAGGAGACAGA 120
 87 AGATGTGACATCCAGATGACCCAGATCTCATCTTCCCTGCTGCTGCTGAGGAGACAGA 146
 121 GTACCATCTACTTGCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 180
 147 GTACCATCTACTTGCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 206
 181 AAACGAGAAAGCTCCTAAGCTCCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
 207 AAACGAGAAAGCTCCTAAGCTCCTGATGATGATGATGATGATGATGATGATGATGATGAT 265
 241 CCATCAAGTTTCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 300
 266 CCATCAAGTTTCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 325
 301 CAGCTGAAGATTGTCGACTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 360
 326 CAGCTGAAGATTGTCGACTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 385
 361 GGCGAGGAGCAAGGTGGAATCAAA 387
 386 GGCGAGGAGCAAGGTGGAATCAAA 412

RESULT 15
 BG341239 921 bp mRNA linear EST 27-FEB-2001
 LOCUS 602463904F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576560 5',
 DEFINITION mRNA sequence.
 ACCESSION BG341239
 VERSION BG341239.1 GI:13147677
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 921)
 AUTHORS NIH-MGC <http://imgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LILCM1289 row: h column: 01
 High quality sequence stop: 732.
 Location/Qualifiers

FEATURES

source

1. 921
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4576560"
 /clone_lib="NIH_MGC_48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pORF7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT

253 a 247 c 229 g 191 t 1 others

ORIGIN

Query Match 82.8%; Score 320.6; DB 10; Length 921;
 Best Local Similarity 91.0%; Pred. No. 5.9e-87;
 Matches 352; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

1 ATGACATGAGGAGTCCCGCTCAGCTCCTGCGGCTCCTTCTGCTGCGGCTCCAGAGTGC 60
 15 ATGACATGAGGAGTCCCGCTCAGCTCCTGCGGCTCCTTCTGCTGCGGCTCCAGAGTGC 74
 61 AGATGTGACATCCAGATGACCCAGATCTCATCTTCCCTGCTGCTGCTGAGGAGACAGA 120
 75 AGATGTGACATCCAGATGACCCAGATCTCATCTTCCCTGCTGCTGCTGAGGAGACAGA 134
 121 GTACCATCTACTTGCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 180
 135 GTACCATCTACTTGCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 194
 181 AAACGAGAAAGCTCCTAAGCTCCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
 195 AAACGAGAAAGCTCCTAAGCTCCTGATGATGATGATGATGATGATGATGATGATGATGAT 253
 241 CCATCAAGTTTCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 300
 254 CCATCAAGTTTCAGGCGCAAGTACGACATTAGTATTAAATTGGTATCAGCAG 313
 301 CAGCTGAAGATTGTCGACTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 360
 314 CAGCTGAAGATTGTCGACTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 373
 361 GGCGAGGAGCAAGGTGGAATCAAA 387
 374 GGCGAGGAGCAAGGTGGAATCAAA 400

Search completed: September 23, 2002, 17:06:57
Job time: 4516 sec

GenCore, version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:58:42 ; Search time 488.47 Seconds

(without alignments)
1360.259 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387
Sequence: 1 ATGCACATGAGGTCGCCG.....GACCCAGCTGGAATCAAA 387

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :
1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	387	100.0	387	19 AAV33309	Anti-human CD23 5E
2	387	100.0	19035	19 AAV61794	Traget Plasmid Man
3	342.2	88.4	729	21 AAA11630	Human Immunoglobul
4	334.2	86.4	336	18 AAT75423	Human anti-tumour
5	334.2	85.1	438	22 AAH41157	Human coding seque
6	329.4	84.3	974	24 AAS99473	Anti-human AILIM m
7	326.2	83.9	714	21 AAA46899	DNA encoding the k
8	324.6	83.9	387	21 AAZ39327	Nucleotide sequenc
9	321.4	83.0	390	21 AAZ39340	Nucleotide sequenc

10	318.2	82.2	388	18 AAT73441	Human immunoglobul
11	318.2	82.2	388	19 AAV39239	Functional kappa t
12	318.2	82.2	388	20 AA21993	Partial nucleotide
13	318	82.2	936	21 AAA27390	Human IGFM-10 imm
14	316.6	81.8	817	21 AAA27389	Human IGFM-9 immu
15	316.6	81.8	1066	14 AAQ49943	Human anti-HBS 11g
16	316.4	81.8	917	21 AAQ27381	Human IGFM-1 immu
17	311.8	80.6	944	22 AAT44892	Human breast cance
18	309.8	80.1	384	21 AAQ39320	Nucleotide sequenc
19	307.8	79.3	387	16 AAQ82749	93K9 anti-Varicel
20	307	79.3	409	19 AAV39241	Functional kappa t
21	307	79.3	439	18 AAT73443	Human immunoglobul
22	306	79.1	387	21 AA339325	Nucleotide sequenc
23	305.4	78.9	439	20 AAT21995	Partial nucleotide
24	304.2	78.6	705	18 AAT61240	Human anti-RSV mon
25	303.8	78.5	389	15 AAQ67194	Humanized 1308F VL
26	303.8	78.5	389	17 AAT16181	Hu1308 VL encoding
27	303.6	78.4	928	21 AA27393	Human IGFM-13 imm
28	302.4	78.1	372	21 AA339326	Nucleotide sequenc
29	302	78.0	420	18 AAT73445	Human immunoglobul
30	302	78.0	420	19 AAV39293	Synthetic kappa 11
31	302	78.0	420	20 AA22047	Nucleotide sequenc
32	302	78.0	3819	18 AAT78825	Kappa light chain
33	302	78.0	3819	19 AAV39266	Plasmid pIC65 nuc
34	302	78.0	3819	20 AA22020	Nucleotide sequenc
35	297.8	77.0	384	21 AAT39339	Nucleotide sequenc
36	297.4	76.8	330	16 AAQ87337	Nucleotide sequenc
37	297	76.7	366	18 AAT79921	Anti-Interleukin-1
38	296.8	76.7	363	23 AAT76095	Immunoglobulin r86
39	296.8	76.7	702	14 AAQ43773	DNA encoding novel
40	296.2	76.5	384	17 AAQ43773	Sequence encoding
41	296.2	76.5	384	18 AAT85844	Monoclonal antibod
42	295	76.2	372	21 AA339322	Nucleotide sequenc
43	293.2	75.8	928	22 AAH26799	Human immune respo
44	292.6	75.6	390	21 AA339336	Nucleotide sequenc
45	292.4	75.6	930	22 AAH31350	Human secreted pro

ALIGNMENTS

AAV33309	1	AAV33309 standard; DNA: 387 BP.
AAV33309	1	AAV33309; (first entry)
18-NOV-1998	1	18-NOV-1998 (first entry)
Anti-human CD23 5E8 monoclonal antibody light chain variable region DNA.	1	Anti-human CD23 5E8 monoclonal antibody; light chain variable region;
Anti-human CD23 5E8 monoclonal antibody; light chain variable region;	1	Anti-human CD23 5E8 monoclonal antibody; light chain variable region;
human CD23; IGE: FcεRII/CD23; gamma-1 constant region;	1	human CD23; IGE: FcεRII/CD23; gamma-1 constant region;
gamma-3 constant region; allergy; inflammation; autoimmune disease;	1	gamma-3 constant region; allergy; inflammation; autoimmune disease;
allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.	1	allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
Macaca fascicularis	1	Macaca fascicularis
Location/Qualifiers	1	Location/Qualifiers
1.387	1	1.387
/*tag- a	1	/*tag- a
/product= "anti-human CD23 5E8 light chain variable region"	1	/product= "anti-human CD23 5E8 light chain variable region"
/note= "CDS does not contain a stop codon"	1	/note= "CDS does not contain a stop codon"
1..66	1	1..66
/*tag- b	1	/*tag- b
67..387	1	67..387
/*tag- c	1	/*tag- c
136..168	1	136..168
/*tag- d	1	/*tag- d
/note= "encodes CDR 1 region"	1	/note= "encodes CDR 1 region"
214..234	1	214..234
/*tag- e	1	/*tag- e
misc-feature	1	misc-feature

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FT      /note- "encodes CDR 2 region"
FT      331..357
FT      /tag- f
FT      /note- "encodes CDR 3 region"
PN      WO9837099-A1.
XX      27-AUG-1998.
XX      17-FEB-1998; 98WO-US02253.
XX      05-FEB-1998; 98US-0803085.
XX      20-FEB-1997; 97US-0803085.
PA      (IDEC-) IDEC PHARM CORP.
PA      (SECK ) SEIRAGAKU CORP.
XX      Kioetzer WS, Nakamura T, Reif ME;
XX      WPI; 1998-467495/40.
DR      P-PsDB; AAW70379.
XX      New anti-human CD23 monoclonal antibody - used for inhibiting Ige
PT      expression to treat or prevent allergic, inflammatory and
PT      auto-immune conditions
XX      Example 1; Pages 106-108; 146pp; English.
XX      The present sequence represents a DNA sequence encoding the light
CC      chain variable region of primate monoclonal antibody anti-human CD23 5F8.
CC      The invention provides primate monoclonal antibodies which specifically
CC      bind human CD23, the low affinity receptor for Ige (FcεRI/CD23),
CC      and comprise either of a human gamma-1 or human gamma-3 constant region
CC      that binds to human Fc gamma receptors and inhibits Ige expression.
CC      The monoclonal antibodies of the invention are claimed to be useful
CC      for inhibiting induced Ige production for treating or preventing
CC      allergic, inflammatory and auto-immune conditions e.g. allergic rhinitis
CC      conjunctivitis, auto-immune haemolytic anaemia, etc.
XX      Sequence 387 BP; 92 A; 102 C; 98 G; 95 T; 0 other:
SQ

```

```

RESULT 2
ID      AAV61794 standard; DNA: 19035 BP.
XX      AAV61794;
XX      07-JUN-1999 (first entry)
DE      Target plasmid Mandy containing anti-CD23 gene.
XX      Mandy; target plasmid; gene integration; gene amplification;
XX      homologous recombination; vector; neomycin phosphotransferase;
KW      neo gene; selectable marker; immunoglobulin; CD23; 5E8; human; ss.
XX      Chimeric - Mus sp.
OS      Chimeric - Escherichia coli.
OS      Chimeric - Baculovirus.
OS      Chimeric - Cytomegalovirus.
OS      Chimeric - Rhesus macaque polyoma virus.
OS      Chimeric - Photinus sp.
OS      Chimeric - Salmonella typhimurium.
XX      Chimeric - Homo sapiens.
XX      Key
FH      Location/Qualifiers
FT      361
FT      misc-feature
FT      /tag-
FT      /note- "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      721
FT      /tag-
FT      /note- "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      2941
FT      /tag-
FT      /note- "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      3301
FT      /tag-
FT      /note- "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc-feature
FT      4261
FT      /tag-
FT      /note- "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc-feature
FT      4621..4622
FT      /tag-
FT      /note- "these bases represent nucleotides missing
FT      from the sequence given in the
FT      specification. They are included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc-feature
FT      8161
FT      /tag-
FT      /note- "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to

```

FT				maintain the nucleotide numbering in the
FT	misc_feature			specification for this sequence"
FT		8521..8522	n	"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
FT		12061	i	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
FT		12421	j	"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
FT		13381	k	"this base represents a nucleotide missing from the sequence given in the specification. It is included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
FT		14641..14642	l	"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
FT		15001..15002	m	"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
FT		15961..15962	n	"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
FT		16321..16322	O	"these bases represent nucleotides missing from the sequence given in the specification. They are included to maintain the nucleotide numbering in the specification for this sequence"
FT	misc_feature			
PN	M09841645-A1.			
PX				
PD	24-SEP-1998.			
XX				
PF	09-MAR-1998:	98WO-US03935.		
XX				
PR	13-FEB-1998:	98US-0022715.		
XX				
PR	14-MAR-1997:	97US-0819866.		
XX				
PA	(IDEC-) IDEC PHARM CORP.			
XX				
PI	Barnett RS, McLachlan KR, Reff ME;			
XX				
R	WPI; 1998-521229/44.			

XX Site specific integration of DNA in mammals for expressing, e.g.
PT Immunoglobulins - comprises homologous recombination using
PT selectable marker and target plasmids.

PS Example 1; Fig 10; 114pp; English.

XX This is the nucleotide sequence of novel target plasmid Mandy.
CC The plasmid includes an inactivated murine dihydrofolate reductase
CC (DHFR) gene, the Escherichia coli beta-galactosidase gene,
CC baculovirus DNA, a cassette comprising the promoter and enhancer
CC elements from cytomegalovirus and SV40 virus, the E. coli
CC beta-glucuronidase (Gus) gene, firefly luciferase gene, an
CC inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)
CC gene and transposon Tn5 neomycin phosphotransferase (neo) gene
CC sequences, In a pBR-derived backbone, and also an anti-human CD23
CC IgE receptor human gamma-1 monoclonal antibody 5E8 gene. The
CC invention provides a novel method for integrating a desired
CC exogenous DNA at a target site within the genome of a mammalian
CC cell via homologous recombination. This involves transfecting the
CC cell with a 'marker plasmid' such as Desmond (see AAV61792), which
CC contains a unique sequence that is foreign to the mammalian cell
CC genome and which provides a substrate for homologous recombination,
CC followed by transfection with a 'target plasmid', such as Mandy
CC or Molly (see AAV61793), containing a sequence which provides for
CC homologous recombination with the unique sequences contained in
CC the marker plasmid, and further comprising a desired DNA that is
CC to be integrated into the mammalian cells, typically an
CC immunoglobulin or other secreted mammalian glycoprotein. The
CC homologous recombination system utilises the neo gene as a
CC dominant selectable marker. The neo gene is split into 3 exons.
CC Exon 3 is present on the marker plasmid and becomes integrated
CC into the host cell genome upon integration of the marker plasmid
CC into the mammalian cells. Exons 1 and 2 are present on the
CC targeting plasmid, and are separated by an intron into which at
CC least one gene of interest is cloned. Homologous recombination
CC of the targeting vector with the integrated making vector results
CC in correct splicing of all 3 exons of the neo gene and expression
CC of a functional neo protein. The method is applicable to all
CC mammalian cells, and can be used to express any type of recombinant
CC protein. The use of a triply spliced selectable marker means that
CC all selected colonies arise from homologous recombination. In
CC addition, the number of colonies that need to be screened to
CC identify high producer clones is reduced. An amplifiable gene can
CC be inserted on integration of the making vector, so that when a
CC gene is targeted to this site, the gene is further enhanced by gene
CC amplification.

XX
XX
XX Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other:

SX

Query Match 100.0% Score 387; DB 19; Length 19035;
Best Local Similarity 100.0%; Pred. No. 3.9e-108; Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCACATGAGGGTCCCGCTCAGCTCCGTGGGGCTTCCTGCTCGTGCTCCAGGTGCC 60
Db 7541 atgscatcaggggtcccgctcagctccgtgggccttccttgctcgtcccaagtgc 7600

QY 61 AGATGTGACATCAGATGACCACCAAGTCTCATTTCCCTGTGTGCATCTGTAGGGACAGA 120
Db 7601 agatgtgacatcacgatgaccacagctcatcttcccctcgtcgaatcttaaggyscaga 7660

QY 121 GTCCACATCACCTTGAGGGGAAGTCAGACATTAAGTAAATTGATACAGAG 180
Db 7661 gtccacctaccttgaagygcaagtcagagacataagtatatttaaatggtatcagcgg 7720

QY 181 AACACGAGAAAAAGCTCTAAGCTCCTGATCTATTGTGATCCAGTTTGACAAGTGGGGGC 240
Db 7721 aaacccagaaaaagcctctaagctcctgatctatgttgcacccaagttgcaaaagtgggttc 7780

QY 241 CCATCAAGGTTTCAGGGCAGTAGGATCTGGGACAGAGTTCTACTCTCACCGCTCAGACGCTCG 300

Db 7781 ccatacaggtcagcgcagtgatctggacagagctcactccacgcctcagcagcctg 7840
 QY 301 CAGCCGAGGATTGTCGAGCTTATCTGCTACAGGTTATAGTACCCCTGGAGGTC 360
 Db 7841 cagccgaagatttgcagctactactgtctacaggttctacagctccctcgagcttc 7900
 QY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
 Db 7901 ggccaagagccaaggtggaatcaaa 7927

RESULT 3
 AA11630
 ID AA11630 standard; DNA; 729 BP.
 XX
 AC AA11630;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Human immunoglobulin light chain kappa region subgroup type I DNA.
 XX
 KW Fas; antibody: human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antineumatic; anti-Fas;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI: 2000-258930/23.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Example 2; Page 154; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antineumatic, nephrotropic, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a human immunoglobulin light chain kappa variable region subgroup type I
 CC which is used in the construction of humanised anti-Fas antibody
 CC constructs described in the method of the invention.
 XX
 XX Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;
 XX

Query Match 88.4%; Score 342.2; DB 21; Length 729;
 Best Local Similarity 92.8%; Pred No. 6e-95;
 Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGTCGCCGCTCAGCTCTGGGGCTTCCTGCTGCTGCTCCAGGTGCC 60
 Db 7 atggacatgagggtcccgctcgtcctcggtggtcctcgtcgtcgtccgaggtgcc 66
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTGTCATCTGAGGACAGA 120
 Db 67 agatgtgacatccagatgacccaagctccatccctcgtcgtcagtcagtgagagacaga 126
 QY 121 GTCCACATCATCTGACGGGCAAGTCAGACATTAGGTATTATTAAATGGTATACAGAG 180
 Db 127 gtccacatcactcgtccgggcaagtcagagcattagagcatttaattgtatcagcag 186
 QY 181 AAACGAGAAAGCTCTTAAGCTCTGATCTATGTATGTTCATCCAGTTGCAAGTGGGTC 240
 Db 187 aaaccgagaaagcccttaagctcctgactatgctgcagtcacagtttgaaagtgggttc 246
 QY 241 CCATCAAGTTCAGCGGCGAGTGGATCTGGGACAGAGTTACCTACCTGACGACACCTG 300
 Db 247 ccatacaggtcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 306
 QY 301 CAGCCGAGGATTGTCGAGCTTATCTGCTACAGGTTATAGTACCCCTGGAGGTC 360
 Db 307 cagccgaagatttgcagctactactgtctacaggttctacaggttccctcgagcttc 366
 QY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387
 Db 367 ggccaagagccaaggtggaatcaaa 393

RESULT 4
 AAT75423
 ID AAT75423 standard; cDNA; 396 BP.
 XX
 AC AAT75423;
 XX
 DT 12-SEP-1997 (first entry)
 XX
 DE Human anti-tumour antigen antibody light chain variable region cDNA.
 XX
 DE Human: tumour antigen; cancer; monoclonal; antibody; light chain;
 KW variable region; medicine; pharmacology; biochemistry; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH sig_peptide 1..66 /*tag= a
 FT mat_peptide 67..396 /*tag= b
 FT
 XX JP09100300-A.
 XX 15-APR-1997.
 PD
 XX

CC variable region, comprising a modified contiguous sequence from a
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The
CC modifications are contained in CDR1, CDR2 and/or framework regions.
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the
CC immune system to treat hyperimmunity disorders (e.g. autoimmune
CC disease, diabetes and graft rejection) and proliferative disorders
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate
CC immune system to up-regulate immunodeficient disorders.

Sequence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;

Query Match 84.3%; Score 326.2; DB 21; Length 714;
Best Local Similarity 90.2%; Pred. No. 4.8e-90;
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```
OY 1 ATGGACATGAGGTCCTCCGCTCAGTCTCTGGGCTCCTTCTGCTGGCTCCAGGTC 60
DB 1 atggacatgaggtctcccgctcagctccctcctggtcctcctgctcagtcgagtgcc 60
OY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTAGGGACAGA 120
DB 61 agatgtgacatccagatgacccagctccatctccctgtcgtcagctgtaggagacaga 120
OY 121 GTCCACATCACTTGCAGGGCAGTCAAGCATTTAGTATTTAATTGCTATCAGCAG 180
DB 121 gtccacatcacttgcaggcagtcagacatgacatgattagattgtagtcagcag 180
OY 181 AAACGAGAAAGCTCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240
DB 181 aaacgagaaagctcttaagctctgactcctgactcctcctcctcctcctcctcctcctc 240
OY 241 CCATCAAGTTTCAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300
DB 241 ccatacaagtttcagcgagtgatgtgagtgatgtgagtgatgtgagtgatgtgagtgatgtg 300
OY 301 CAGCCTGAGATTTCGAGTCTTACTGCTCTACAGTTTATAGTACCCCTCGAGAGTTC 360
DB 301 cagcctgaagatttcgagcttactgctctacagtttatagtacccctcgagagtttc 360
OY 361 GGCCAAAGGACCAAGTGTGAATCAAA 387
DB 361 ggcctgaggaaccaagtggaatcaaa 387
```

RESULT 8

AAZ39327
ID AAZ39327 standard; DNA; 387 BP.

AC AAZ39327;

DT 15-FEB-2000 (first entry)

DE Nucleotide sequence of chimpanzee V kappa CDNA clone 46-14.

KM Complementarity determining region; antibody; primate; immunogenicity;

KW Old World ape; Old World monkey; antigen-binding affinity; ss.

OS Pan troglodytes.

PN WO955369-A1.

PD 04-NOV-1999.

PF 28-APR-1999; 99WO-US09131.

PR 28-APR-1998; 98US-0083367.

PA (SMK) SMITHKLINE BEECHAM CORP.

PI Taylor AH;

DR WPI; 2000-023265/02.

DR P-PSDB; AAY56659, AAY56724.

XX

PT Antibodies containing donor complementarity determining regions and

PS non-human primate acceptor frameworks, having reduced immunogenicity in

XX humans -

XX

XX

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XX

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Example 2; Page 67-68; 123pp; English.

CC The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarity determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.

Sequence 387 BP; 94 A; 104 C; 95 G; 94 T; 0 other;

Query Match 83.9%; Score 324.6; DB 21; Length 387;
Best Local Similarity 89.9%; Pred. No. 1.2e-89;
Matches 348; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
OY 1 ATGGACATGAGGTCCTCCGCTCAGTCTCTGGGCTCCTTCTGCTGGCTCCAGGTGCC 60
DB 1 atggacatgaggtctcccgctcagctccctcctggtcctcctgctcgtcgtcagtgacc 60
OY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGAGGGACAGA 120
DB 61 agatgtgacatccagatgacccagctccatctccctgtcgtcagctgtaggagacaga 120
OY 121 GTCCACATCACTTGCAGGGCAGTCAAGCATTTAGTATTTAATTGCTATCAGCAG 180
DB 121 gtccacatcacttgcaggcagtcagacatgacatgattagattgtagtcagcag 180
OY 181 AAACGAGAAAGCTCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 240
DB 181 aaacgagaaagctcttaagctctgactcctgactcctcctcctcctcctcctcctcctc 240
OY 241 CCATCAAGTTTCAGCGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300
DB 241 ccatacaagtttcagcgagtgatgtgagtgatgtgagtgatgtgagtgatgtgagtgatgtg 300
OY 301 CAGCCTGAGATTTCGAGTCTTACTGCTCTACAGTTTATAGTACCCCTCGAGAGTTC 360
DB 301 cagcctgaagatttcgagcttactgctctacagtttatagtacccctcgagagtttc 360
OY 361 GGCCAAAGGACCAAGTGTGAATCAAA 387
DB 361 ggcctgaggaaccaagtggaatcaaa 387
```

RESULT 9

AAZ39340
ID AAZ39340 standard; DNA; 390 BP.

AC AAZ39340;

DT 15-FEB-2000 (first entry)

DE Nucleotide sequence of Cynomolgus V kappa CDNA clone 4-10.

KM Complementarity determining region; antibody; primate; immunogenicity;

KW Old World ape; Old World monkey; antigen-binding affinity; ss.

OS Macaca cynomolgus.

PN WO955369-A1.

PD 04-NOV-1999.

XX

Db 361 ggcaggggaccgaagctggagatcaaa 387
|||||
RESULT 11
ID AAV39239 standard; DNA: 388 BP.
AAV39239;
AAV39239;
18-DEC-1998 (first entry)
Functional kappa transcript isolated from transgenic cell line 10C5.
Transgenic animal; human heterologous antibody; transgene;
isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
autoimmune reaction; inflammatory response; transplant rejection;
acid induced lung injury; acute adult respiratory distress syndrome;
ARDS; vasculitis; septic shock; allergic reaction; asthma;
cystic fibrosis; ss.
Synthetic.
Mus sapiens.
Mus sp.
W09824884-A1.
11-JUN-1998.
01-DEC-1997; 97MO-US21803.
02-DEC-1996; 96US-0758417.
(GENP-) GENPHARM INT.
Kay RM, Lonberg N;
MPI: 1998-333306/29.
Hybridoma producing antibody specific for interleukin-8 - used to prevent efflux of neutrophils from vasculature, and treat reperfusion injury
Example 41; Page 304; 452pp; English.
AAV39232-41 represent functional transcripts of a human Igkappa anti-CD4 antibody. The sequences are isolated from 5 different transgenic mouse hybridoma cell lines. The specification describes transgenic non-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals have human heavy and light chain transgenes. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a variable-diversity-junction (V-D-J) recombination. The transgenes included a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V and J gene segment and one constant region gene segment. The gene segments are heterologous to the transgenic animal. The antibody can be used to prevent efflux of neutrophils from vasculature. It can also be used to treat reperfusion injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The anti-IL-8 antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and acid induced lung injury. The anti-IL-8 antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions (e.g. asthma) and cystic fibrosis.
Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;

Query Match 82.2%; Score 318.2; DB 19; Length 388;
Best Local Similarity 88.9%; Pded. No. 1.1e-87;

	Matches	344;	Conservative	0;	Mismatches	43;	Indels	0;	Gaps	0;
Qy	1	ATGGACATGAGAGGCTCCCGGCTACGCTCCGTGGGGCTTCCTGCTGGCTCCAGAGTGGC	60							
Db	1	atggacatgataggctcccgctcaagctccctgggctccgctgcttggctcccaagttcc	60							
Qy	61	AGATGTGACATCCAGATACCCAGTCTCCATCTCCCTGTGTGCATGTGTAGGGACAGA	120							
Db	61	agatgtgacatccagataccagctccatcttcctgctgcatctgttagggagacaga	120							
Qy	121	GTGACCATCTCTGCGAGGGCAAGTACGACATATAGTATATTAAATTTGGTATACGAC	180							
Db	121	gtcacccatctctgctcggcgagatcagaatatagcaagctglttagccgtgatacgaat	180							
Qy	181	AAACGAGGAAAAAGCTCTAAGCTCCTGATCTATTTGGATCCAGATTGGCAAGTGGGGTC	240							
Db	181	aaacgaggaagagccccaagctcctgaactctatgctgcacatcgaattgcaaaagtgggtc	240							
Qy	241	CCATCAAGGTTACGCGGAGTGTGATCTGGGACAGATTCACTCACTCAGCCGTACGACCTG	300							
Db	241	ccatcaaggttcagcggcaggtgcatctcgagacagattcaacttcacatcagcagcctg	300							
Qy	301	CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGAGTTTATAGTACCCCTCGGACGTT	360							
Db	301	cagcctgaagatcttgcacaacttactatctgccaacagcgttaaatagttcccgtaacattt	360							
Qy	361	GGGCAGGAGGACCAAGTGGAATCAAA	387							
Db	361	ggccaggaggaccaaagctggaagataaa	387							

RESULT	12
ID	AAZ21993
XX	AAZ21993 standard; DNA; 388 BP.
AC	AAZ21993;
XX	
DT	24-NOV-1999 (first entry)
XX	
DE	Partial nucleotide sequence for a functional transcript 10C5-kappa.
XX	
KW	Transgenic animal; heterologous antibody; hybridoma; B cell;
KW	transgenic mouse; human heavy chain transgene; diroxin; PCR primer;
KW	human light chain transgene; immortalized cell; immunoglobulin;
KW	Shunga-like toxin; autoimmune disease; cancer; infectious disease;
XX	transplant rejection; blood disorder; coagulation disorder; ss.
OS	Synthetic.
OS	Homo sapiens.
PN	W09945962-A1.
XX	
PD	16-SEP-1999.
XX	
PF	12-MAR-1999; 99WO-US05535.
XX	
PR	13-MAR-1998; 98US-0042353.
PA	(GENP-) GENPHARM INT INC.
XX	
PI	Lomberg N, Fishwild DM, Ball WJ;
XX	
DR	WPI: 1999-551219/46.
XX	
PT	Novel transgenic non-human animals used to produce heterologous
PT	antibodies
XX	
PS	Example 41; Page 305; 484pp; English.
CC	The specification describes transgenic animals that are capable of
CC	producing a heterologous antibody. The antibodies are isolated from a
CC	hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC	having a genome comprising a human heavy chain transgene and a human

RESULT 14
 ID AAA27389
 AAA27389 standard; cDNA: 817 BP.
 AA27389;
 16-AUG-2000 (first entry)
 Human IGFAM-9 immunoglobulin coding sequence.
 Human; Immunoglobulin; IGFAM-9; IGFAM; immune disorder; cancer;
 Infection; Inflammation; haematopoiesis; AIDS; allergy; ss.
 Homo sapiens.

Key	Location/Qualifiers
CDS	11..721
FT	/*tag= a
FT	/product= "IGFAM-9"
FT	11..76
FT	/*tag= b
FT	77..718
FT	/*tag= c

 WO200029583-A2.
 25-MAY-2000.
 19-NOV-1999; 99WO-US27566.
 19-NOV-1998; 99US-0113635.
 22-DEC-1998; 98US-0113635.
 07-APR-1999; 99US-0128194.
 (INCY-) INCYTE PHARM INC.
 Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
 Lu DAM, Lal P, Hillman JL, Yang J;
 WPI: 2000-387796/33.
 P-PSDB: AAY96297.
 Immunoglobulin superfamily proteins, the agonist and antagonist of the
 protein is useful for preventing and treating disorders associated with
 altered levels of the protein such as cancer, immune system disorders
 Claim 9; Page 99; 105pp; English.
 The present sequence is the human immunoglobulin superfamily protein
 IGFAM-9 gene, which was isolated from a cDNA library of breast tumour
 tissue. It is expressed in reproductive, gastrointestinal and immune
 and haematopoietic tissue, where cancer and inflammation are common. The
 gene, protein, its antibodies, agonists and antagonists are suitable for
 diagnosing and treating many diseases, including cancer, immune system
 disorders (such as inflammation, AIDS, allergies, anaemia,
 arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
 disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
 multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
 systemic lupus erythematosus and ulcerative colitis), complications of
 cancer, haemodialysis and extracorporeal circulation, trauma and
 haematopoietic cancer (such as leukaemia) and infections caused by
 bacteria, viruses, fungi or parasites.
 Sequence 817 BP; 202 A; 237 C; 197 G; 181 T; 0 other;

OY	1	ATGGACATGAGAGGATCCCGGCTCAGCTCTCGGGGCGCTTTCGCTGAGGCCAGGAGGCC	60
Db	11	atggacatgagagatccctgcgcacagctccctgggctccctgcgcgcgtcttcccaaggcc	70
OY	61	AGATGTGACATCCAGATGACCAGCTCTCCATCTTCCCTGTCGATGTGATGAGGGACAGA	120
Db	71	agatgtgacatccagatgaccagctctccatccatccacgtctgatctgttggagacaga	130
OY	121	GTCCACATCACTTGCAGGGCAAGTCAGACACTTATGATATTTAAATTGGTATCACAG	180
Db	131	gtccacatcactctgcggcgagatcagacatattagactgttgcagcag	190
OY	181	AAACGAGGAAAAAGCCTCACTCCTGTATATGTGATCAGCACTTGGCAAGGCGGTC	240
Db	191	aaacgaggaacagcccccagaatccctgcgtcatgataatccagcttgcagaagtgggctc	250
OY	241	CCATCAAGGTTTCAGCGGACAGTGTGGGACAGAGTTTCACTCTCACCGTACGACGCTG	300
Db	251	ccatcaaggttcagggcgagtgatctcgtggcagatctcactctcacatcaacaagctcg	310
OY	301	CAGCTGAAGATTTTGCACATTATTACTGTTACAGGTTTATGATACCCCTCGGACGCTC	360
Db	311	cagctgaagatcttgcacaattatcactgcacaacagcatagatatactccttactcttc	370
OY	361	GGCCAAAGGACCAAGGTGGAATCAA	387
Db	371	ggccgaaggaccaagtgagatcaaa	397

RESULT	15
AA049943	
ID	AA049943 standard; cDNA; 1066 BP.
XX	
AC	AA049943;
XX	
DT	29-APR-1994 (first entry)
XX	
DE	Human anti-HBs light chain.
XX	
KW	Antibody; Ab; light; heavy; chain; hepatitis B;
KW	HB; surface antigen; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
CD	Location/Qualifiers
FT	33..743
FT	/*tag- a
FT	sig_peptide
FT	33..98
FT	/*tag- b
FT	mat_peptide
FT	99..740
FT	/*tag- c
FT	/note= "claim 1, page 26"
XX	
PN	W09320205-A.
XX	
PD	14-OCT-1993.
XX	
PF	30-MAR-1993; 93MO-JP00396.
XX	
PR	30-MAR-1992; 92JP-0074678.
XX	
PPA	(SUNR) SUNTORY LTD.
XX	
PI	Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;
XX	
DR	WPI; 1993-336913/42.
DR	P-PSDB; AAR42065.
XX	
PT	Human anti-hepatitis B surface antigen antibody gene - can be
XX	used to produce L and H chains of the antibody in large quantity
PS	Disclosure; Fig 4-5; 46pp; Japanese.
XX	

CC Polynucleotides encoding the L and H chains of human anti-HBs
CC Ab are given in AA049943-049944. The Ab can be easily produced in
CC large quantities for therapeutic use.
XX
SQ Sequence 1066 BP; 338 A; 274 C; 240 G; 214 T; 0 other;

```
Query Match      81.8%; Score 316.6; DB 14; Length 1066;
Best Local Similarity 88.6%; Pred. No. 4..9e-87;
Matches 343; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGACACTGAGGGTCCCGGCTCAGCTCTGGGCTCCTTCTGCTCTGCTCCAGTGCC 60
    |||||||
DB 33 atggacatgaggggtcccgctcagctctgggctccttctgctctgctccagtgcc 92
    |||||||

QY 61 AGATGTGACATCCAGATGACCCAGTTCATCTCCCTGCTGATCTGTAGGGACAGA 120
    |||||||
DB 93 aggtgtgacatccagatgacccagttccatctcgcatgctgtaggagacaga 152
    |||||||

QY 121 GTCAACCATCTTGACAGGCAAGTCAGACATTAGTATTAAATGGTATCAGCAG 180
    |||||||
DB 153 gtcaaccatctgtcgagcgagtcagagtcagcaattatctagtcgttcagcag 212
    |||||||

QY 181 AAACGAGAAAGCTCCTAGCTCCTGATCTATGTTGATCCAGTTGCAAGTGGGTC 240
    |||||||
DB 213 aaacgaggaagctccctaagcgctgatactatgctcaccagttcgcaagtcgggctc 272
    |||||||

QY 241 CCATCAAGTTTCAGCGGAGTGTGATCTGGAGAGTTCACTCCACCGTCAGCGCCTG 300
    |||||||
DB 273 ccatacgaggttcagcgagtcgagtcgagacagaattcactccacaatcagcagactg 332
    |||||||

QY 301 CAGCCTGAAGATTTTGGCACTTATTACTGCTACAGGTTTATAGTACCCTCGGACGTTT 360
    |||||||
DB 333 cagcctgaagatlttgcaacttactgtacatacataataataaccgctaagtttc 392
    |||||||

QY 361 GGCCAAGGACCAAGTGGAATCAAA 387
    |||
DB 393 ggcgagggaccaaagtcgagatcaaa 419
    |||||||
```

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Job time: 7014 sec

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:47:18 ; Search time 6364.12 Seconds

(without alignments)
1315.611 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGCACATGAGCGTCCCGC.....GACCACAGGTGAATCAAA 387

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents, NA, Main:*

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2: /cgn2_6/ptodata/1/pna/US06_COMB.seq.*
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4: /cgn2_6/ptodata/1/pna/US08_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US081_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US082_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US083_COMB.seq.*
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16: /cgn2_6/ptodata/1/pna/US092_COMB.seq.*
17: /cgn2_6/ptodata/1/pna/US093_COMB.seq.*
18: /cgn2_6/ptodata/1/pna/US094_COMB.seq.*
19: /cgn2_6/ptodata/1/pna/US095A_COMB.seq.*
20: /cgn2_6/ptodata/1/pna/US095B_COMB.seq.*
21: /cgn2_6/ptodata/1/pna/US095C_COMB.seq.*
22: /cgn2_6/ptodata/1/pna/US095D_COMB.seq.*
23: /cgn2_6/ptodata/1/pna/US096A_COMB.seq.*
24: /cgn2_6/ptodata/1/pna/US096B_COMB.seq.*
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27: /cgn2_6/ptodata/1/pna/US096E_COMB.seq.*
28: /cgn2_6/ptodata/1/pna/US097A_COMB.seq.*
29: /cgn2_6/ptodata/1/pna/US097B_COMB.seq.*
30: /cgn2_6/ptodata/1/pna/US097C_COMB.seq.*
31: /cgn2_6/ptodata/1/pna/US098A_COMB.seq.*
32: /cgn2_6/ptodata/1/pna/US098B_COMB.seq.*
33: /cgn2_6/ptodata/1/pna/US098C_COMB.seq.*
34: /cgn2_6/ptodata/1/pna/US099A_COMB.seq.*
35: /cgn2_6/ptodata/1/pna/US099B_COMB.seq.*
36: /cgn2_6/ptodata/1/pna/US099C_COMB.seq.*
37: /cgn2_6/ptodata/1/pna/US100_COMB.seq.*
38: /cgn2_6/ptodata/1/pna/US101_COMB.seq.*
39: /cgn2_6/ptodata/1/pna/US6000_COMB.seq.*
40: /cgn2_6/ptodata/1/pna/US6001_COMB.seq.*
41: /cgn2_6/ptodata/1/pna/US6002_COMB.seq.*
42: /cgn2_6/ptodata/1/pna/US6003_COMB.seq.*
43: /cgn2_6/ptodata/1/pna/US6004_COMB.seq.*

Result				Query				SUMMARIES				Description			
No.	Score	Match	Length	DB	ID										
1	387	100.0	387	14	US-09-019-441-3							Sequence 3, Appl			
2	387	100.0	387	16	US-09-292-053-5							Sequence 5, Appl			
3	387	100.0	19040	17	US-09-343-485A-3							Sequence 3, Appl			
4	342.2	88.4	729	18	US-09-408-646-125							Sequence 125, Appl			
5	342.2	88.4	1209	18	US-09-499-662-125							Sequence 125, Appl			
6	339	87.6	1106	1	PCT-US01-18569-121							Sequence 121, Appl			
7	335.2	86.6	812	30	US-09-760-479-405							Sequence 405, Appl			
8	331.8	85.7	500	32	US-09-834-366-44							Sequence 44, Appl			
9	331.8	85.7	500	58	US-09-197-873-44							Sequence 44, Appl			
10	329.4	85.1	974	32	US-09-859-053-29							Sequence 29, Appl			
11	327.8	84.7	974	30	US-09-760-479-192							Sequence 192, Appl			
12	327	84.5	391	16	US-09-289-768-2087							Sequence 2087, Appl			
13	327	84.5	391	35	US-09-939-397-2087							Sequence 2087, Appl			
14	326.2	84.3	549	26	US-09-665-486-816							Sequence 816, Appl			
15	326.2	84.3	549	55	US-09-168-599-218							Sequence 218, Appl			
16	326.2	84.3	714	18	US-09-472-087-62							Sequence 62, Appl			
17	324.6	83.9	387	1	PCT-US99-09131-27							Sequence 27, Appl			
18	324.6	83.9	387	17	US-09-300-970A-27							Sequence 27, Appl			
19	324.6	83.9	387	34	US-09-905-243-27							Sequence 27, Appl			
20	323	83.4	728	32	US-09-844-684-15							Sequence 15, Appl			
21	322.8	83.4	408	17	US-09-362-510A-22815							Sequence 22815, A			
22	322.8	83.4	408	17	US-09-362-510A-22815							Sequence 22815, A			
23	322.8	83.4	408	34	US-09-904-013-22815							Sequence 22815, A			
24	321.8	83.2	474	32	US-09-834-366-31							Sequence 31, Appl			
25	321.8	83.2	474	58	US-09-197-873-31							Sequence 31, Appl			
26	321.6	83.1	402	19	US-09-528-409-22604							Sequence 22604, A			
27	321.6	83.1	402	35	US-09-933-524A-22604							Sequence 22604, A			
28	321.6	83.1	402	35	US-09-933-524A-22604							Sequence 22604, A			
29	321.4	83.0	390	1	PCT-US99-09131-57							Sequence 57, Appl			
30	321.4	83.0	390	17	US-09-300-970A-57							Sequence 57, Appl			
31	321.4	83.0	390	34	US-09-905-243-57							Sequence 57, Appl			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

32 321.4 83.0 514 1 PCT-US02-02870-2025 Sequence 2025, Ap
33 321.4 83.0 514 37 US-10-066-543-2025 Sequence 2025, Ap
34 321.4 83.0 537 1 PCT-US02-02870-186 Sequence 186, App
35 321.4 83.0 537 37 US-10-066-543-186 Sequence 186, App
36 321.4 83.0 716 32 US-09-844-684-13 Sequence 13, App1
37 320.8 82.9 397 19 US-09-528-409-22603 Sequence 22603, A
38 320.8 82.9 397 35 US-09-933-524-22603 Sequence 22603, A
39 320.8 82.9 397 35 US-09-933-524-22603 Sequence 22603, A
40 318.2 82.2 388 11 US-08-728-463-206 Sequence 206, App
41 318.2 82.2 388 11 US-08-728-463-206 Sequence 206, App
42 318.2 82.2 388 29 US-09-724-965-206 Sequence 206, App
43 318.2 82.2 415 16 US-09-274-861-8123 Sequence 8123, App
44 318.2 82.2 415 34 US-09-915-738-8123 Sequence 8123, App
45 318 82.2 936 50 US-60-113-635-20 Sequence 20, App1

ALIGNMENTS

RESULT 1
US-09-019-441-3
Sequence 3, Application US/09019441
GENERAL INFORMATION:
APPLICANT: REF, MITCHELL E.
KLOETZER, WILLIAM S.
NAKAMURA, TAKEHIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..387
NAME/KEY: mat_peptide
LOCATION: 67..387
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-019-441-3

Query Match 100.0%; Score 387; DB 14; Length 387;

Best Local Similarity 100.0%; Pred. No. 7.5e-109;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCAGGTGC 60
1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCAGGTGC 60
Db 1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCAGGTGC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGGACAGA 120
61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGGACAGA 120
QY 121 GTCACCATCCTTGTGAGGGGCAAGTACAGACATTTATTTAAATTGGTATACAGC 180
121 GTCACCATCCTTGTGAGGGGCAAGTACAGACATTTATTTAAATTGGTATACAGC 180
Db 121 GTCACCATCCTTGTGAGGGGCAAGTACAGACATTTATTTAAATTGGTATACAGC 180
QY 181 AAACGAGAAAAGCTCTAGCTCCTGATCTATGTGATCAGTTCCAAAGTGGGGTC 240
181 AAACGAGAAAAGCTCTAGCTCCTGATCTATGTGATCAGTTCCAAAGTGGGGTC 240
Db 181 AAACGAGAAAAGCTCTAGCTCCTGATCTATGTGATCAGTTCCAAAGTGGGGTC 240
QY 241 CCATCAGGTTTCAGGCGAGTGATCTGGACAGAGTTCACTCTCACCGTCAGACCTG 300
241 CCATCAGGTTTCAGGCGAGTGATCTGGACAGAGTTCACTCTCACCGTCAGACCTG 300
Db 241 CCATCAGGTTTCAGGCGAGTGATCTGGACAGAGTTCACTCTCACCGTCAGACCTG 300
QY 301 CAGCTGAAGATTITGGCAGCTTATTACTGTCTACAGGTTTAAATGATCCCTGGACGTTG 360
301 CAGCTGAAGATTITGGCAGCTTATTACTGTCTACAGGTTTAAATGATCCCTGGACGTTG 360
Db 301 CAGCTGAAGATTITGGCAGCTTATTACTGTCTACAGGTTTAAATGATCCCTGGACGTTG 360
QY 361 GGCCAGGACCAAGGTGGAATCAA 387
361 GGCCAGGACCAAGGTGGAATCAA 387
Db 361 GGCCAGGACCAAGGTGGAATCAA 387

RESULT 2
US-09-292-053-5
Sequence 5, Application US/09292053
GENERAL INFORMATION:
APPLICANT: REF, MITCHELL E.
KLOETZER, WILLIAM S.
NAKAMURA, TAKEHIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
FILE REFERENCE: 23522.0699
CURRENT APPLICATION NUMBER: US/09/292,053
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 08/803,085
PRIOR FILING DATE: 1997-02-20
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 387
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(67)
NAME/KEY: mat_peptide
LOCATION: (67)..(387)
NAME/KEY: CDS
LOCATION: (1)..(387)
US-09-292-053-5

Query Match 100.0%; Score 387; DB 16; Length 387;
Best Local Similarity 100.0%; Pred. No. 7.5e-109;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCAGGTGC 60
1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCAGGTGC 60
Db 1 ATGGACATGAGGTCCTCCGCTCAGCTCCCTGGGGCTCCTTCTGCTGGCTCCAGGTGC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGGACAGA 120
61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGGACAGA 120
Db 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGATCTGTAGGGGACAGA 120

QY	121	GTACACATCACTTTCAGAGGCAAGACAGACTATGATATTATTTAAATTCGTTACAG	180
QY	121	gtacacatcaacttcgacggcgaagtcagagacatctgagatataatattgatactgacgag	180
Db	121	gtacacatcaacttcgacggcgaagtcagagacatctgagatataatattgatactgacgag	180
QY	181	AAACCCAGGAAAAAGCTCCTAAGCTTCGTATCTATGTTCATCCATCCAGTTTGGCAAAGTGGGGTC	240
Db	181	aaacccaggaaaaagctcctaaagcttcctatcatgtctgacacaglttgcaaaagtggggtc	240
QY	241	CCATCCAGGTTCCACGCGGAGTGTGGGACAGACTTCACCTCCACGTCAGACAGCTG	300
Db	241	ccatccaggttccacgcgagtgagttctgggacagagttcaacttcacgcgtcagagaagctg	300
QY	301	CAGCCTGAGATTTTGGCACTTATTACTGTCFACAGGTTTATATAGTACCCCTCGACGCTTC	360
Db	301	cagcctgagatttggcacttattactgctctacaggtttatagttaccctctgagagcttc	360
QY	361	GGCCAGGAGACCAAGTGGGAATTAATAA	387
Db	361	ggccaaaggagaccaaagtcggaataataa	387

RESULT 3

```

1  Sequence 3 Application US/09343485A
2  GENERAL INFORMATION:
3  APPLICANT: REEF, MITCHELL R.
4  APPLICANT: BARNETT, RICHARD S.
5  APPLICANT: MCLACHLAN, KAREN R.
6  TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
7  TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
8  TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
9  FILE REFERENCE: 037003-0275807
10 CURRENT APPLICATION NUMBER: US/09/343,485A
11 CURRENT FILING DATE: 1999-06-30
12 PRIOR APPLICATION NUMBER: 09/023,715
13 PRIOR FILING DATE: 1998-02-13
14 PRIOR APPLICATION NUMBER: 08/819,866
15 PRIOR FILING DATE: 1997-03-14
16 NUMBER OF SEQ ID NOS: 3
17 SOFTWARE: PatentIn Ver. 2.1
18 SEQ ID NO 3
19 LENGTH: 19040
20 TYPE: DNA
21 ORGANISM: Artificial Sequence
22 FEATURE:
23 OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
24 OTHER INFORMATION: referred to as "Mandy"
25 US-09-343-485A-3

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Query Match	100.0%;	Score 387;	DB 17;	Length 19040;
Best Local Similarity	100.0%;	Pred. No. 3.2e-108;		
Matches 387;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

Db 7785 ccatacaaggttcaagcgcgcagttgactctggagacaggttcaactctcaacgctcaagcagccg 7844

QY 301 CAGCTGAGATTTTGGGACTTTATTCGTCTCAGAGTTTATAGTACCCCTGGAGATTTC 360

Db 7845 cagctcgaagattttggaacttactctactcgtctcagaattatcagtcacccctcgagacttc 7904

QY 361 GGCTAAGGACCAAGGTGTAATCAAA 367

Db 7905 ggcacaggacacaggtcgaatactaa 7931

RESULT 4

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? Sequence 125, Application US/09/4008646A
? GENERAL INFORMATION:
? APPLICANT: Serizawa, Nobufusa
? APPLICANT: Haryuzaki
? APPLICANT: Nakahara, Kaori
? APPLICANT: Tamaki, Ikuko
? APPLICANT: Takahashi, Tohru
? TITLE OF INVENTION: Anti-Fas Antibodies
? FILE REFERENCE: 990540/HG
? CURRENT APPLICATION NUMBER: US/09/4008, 646A
? CURRENT FILING DATE: 1999-09-30
? EARLIER APPLICATION NUMBER: JP 10-276881
? EARLIER FILING DATE: 1998-09-30
? NUMBER OF SEQ ID NOS: 165
? SEQ ID NO 125
? LENGTH: 729
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-408-646-125

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Query Match	88.48;	Score 342.2;	DB 18;	Length 729;
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OY	1	ATASGACATGAGAGGTCGCCGCGACGCTCCTGGGGGTCCTTCGCTGGCTGCCAGGATGCC	60
Db	7	atgagcaatgaaaggtctcccgcctcgtccctggggctccctgtaacctctggtctccgaagtccc	66
OY	61	AGATGTGACATCCAGATGATACCAGATCTTCATCTTCCTCGTGTGCATCTGTAGGGGACAGA	120
Db	67	agatgtgacatccagatgatacccaagtcttcatactccctcgtctgcatctgtatgagagaaaga	126
OY	121	GTACACCATCTACTGCAGGGCAAGTTCAGAGCATTAAGTATTATTTAAATTGGTATCACAG	186
Db	127	gtcaccaactactctgcgggcgaagtcagatcagcaatttaaatgtgtatcagaag	186
OY	181	AAACAGGAAAAAGCTCCCTAACCTCCTGATCTATGTGATCCATCCATTTGCCAAAGTGGGTC	246
Db	187	aaaccaaaggaagagccccaagctccctgtactatgctgataccaagtttgcacaagtggggtc	246
OY	241	CCATCAAGGTTTCAGCGGACAGTGTCTGTGGACAGATGTCATCTCCACGGTACGACGCTG	306
Db	247	ccatcaaggttcagttggaagtgtatcttggggcagaattcaatcccaatcaatcaagagcttc	306
OY	301	CAGCTGAAGATTTTGGCATTATTACTGTCTACAGGTTTATAGTACCCCTGGAGCTTC	366
Db	307	caacctgaagatttttgcactactactactgtcaacaagattacagttacccctcgaagcttc	366
OY	361	GGCCAGGACCAAGGTGGAAATCAAA	387
Db	367	ggccaaggtaccgaagtgtgaaatcaaa	393

RESULT 5

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US-09-499-662-125
; Sequence 125, Application US/09499667
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Hattuyama, Hideyuki
```

```

RESULT      6
PCT-US01-18569-121
; Sequence 121, Application PC/TUS0118569
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA133PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209, 467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ. ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 1106
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (302)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (424)

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Query Match	86.68;	Score 335.2;	DB 30;	Length 812;
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QY 241 CCATCAGGTTTCAGCGGACGTGATCTGGGACAGATTTCACCTCTCACCGTCAGACGCTG 300
      |||
Db 268 ccataaagtgctgagtgatctggtgacagattcactctcaccacacagcagctc 327
QY 301 CACCTGAGAGATTTTGGAGCTTATCTGCTCAGCTTATAGTACCCCTCGAGCTTC 360
      |||
Db 328 caaccggaagattctgcwagtgatctgacacagagtgacaglyccccctmmsackty 387
QY 361 GGCCAAGGACCAAGGTGGAATCAAA 387
      |||
Db 388 ggcctmrggagcaagktgagatcarr 414
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```
RESULT 10
US-09-859-053-29
; Sequence 29, Application US/09859053
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hoil, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig-peptide
; LOCATION: (39)...(104)
US-09-859-053-29
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Query Match 85.1%; Score 329.4; DB 32; Length 974;
Best Local Similarity 90.7%; Pred. No. 7.4e-91;
Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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QY 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGCTGCCAGGCGCC 60
      |||
Db 39 atggaatgaggggtccctcagctcctggtggtccctcgtggtccaggttcc 98
QY 61 AGATGTGACATCAGATGACCCAGTCTCCATCTTCCCTGCTCATCTGTAGGGAGACA 120
      |||
Db 99 agatggaatcctcagatgacccagctcctcctcgtggtcctcgtcagatgagagaga 158
QY 121 GTGACCATCACTTGACGGGCAAGTACAGACATTAGTATTATTAAATGGTATCAGCAG 180
      |||
Db 159 gtacacatcactgtcgtggtcaggtatgacaggtgtgtaagcctgtatcagcag 218
QY 181 AAACGAGAAAGCTCTTAAGTCTGTATCTATGTGATCAGTTGCAAGTGGGGTC 240
      |||
Db 219 aaacagaggaagccctaaacccatcgtatcgtcagctcagttgcaagtggtggtc 278
QY 241 CCATCAGGTTTCAGCGGACGTGATCTGGGACAGATTTCACCTCTCACCGTCAGCCTG 300
      |||
Db 279 ccataaagtgctgagtgatctggtgacagattcactctcaccacacagcagctc 338
```

```
QY 301 CACCTGAGAGATTTTGGAGCTTATCTGCTCAGCTTATAGTACCCCTCGAGCTTC 360
      |||
Db 339 cagcctgaagattctgcaactactatctgacacagagtgtaacaggttccgtgagcttc 398
QY 361 GGCCAAGGACCAAGGTGGAATCAAA 387
      |||
Db 399 ggcgaagggacaaagtggaalcaaa 425
```

```
RESULT 11
US-09-760-479-192
; Sequence 192, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 192
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-760-479-192
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Query Match 84.7%; Score 327.8; DB 30; Length 974;
Best Local Similarity 90.4%; Pred. No. 2.3e-90;
Matches 350; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGCTGCCAGGCGCC 60
      |||
Db 16 atggaatgaggggtccctcagctcctcgtggtggtccctcgtcactcgtcctcaggttcc 75
QY 61 AGATGTGACATCAGATGACCCAGTCTCCATCTTCCCTGCTCATCTGTAGGGAGACA 120
      |||
Db 76 agatggaatcctcagatgacccagctcctcctcgtcgtcgtcgtcgtgagagaga 135
QY 121 GTGACCATCACTTGACGGGCAAGTACAGACATTAGTATTATTAAATGGTATCAGCAG 180
      |||
Db 136 gtacacatcactgtcgtggtcaggtatgacaggtatgacacacatgagtgatcagcag 195
QY 181 AAACGAGAAAGCTCTTAAGTCTGTATCTATGTGATCAGTTGCAAGTGGGGTC 240
      |||
Db 196 aaacagaggaagccctaaacccatcgtatcgtgacagattcactctcaccacagcagctc 255
QY 241 CCATCAGGTTTCAGCGGACGTGATCTGGGACAGATTTCACCTCTCACCGTCAGCCTG 300
      |||
Db 256 ccataaagtgctgagtgatctggtgacagattcactctcaccacagcagctc 315
QY 301 CACCTGAGAGATTTTGGAGCTTATCTGCTCAGCTTATAGTACCCCTCGAGCTTC 360
      |||
Db 316 caaccggaagattctgcaactactatctgacacagagtgtaacacatcctccacttlt 375
QY 361 GGCCAAGGACCAAGGTGGAATCAAA 387
      |||
Db 376 ggcgaagggacaaagtggaalcaaa 402
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RESULT 12
US-09-289-768-2087
; Sequence 2087, Application US/09289768
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-765
; CURRENT APPLICATION NUMBER: US/09/289,768
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 39996
; SOFTWARE: FastSeq for Windows Version 3.0
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SEQ ID NO 2087
LENGTH: 391
TYPE: DNA
ORGANISM: Homo sapiens
US-09-289-768-2087

Query Match 84.5%; Score 327; DB 16; Length 391;
Best Local Similarity 90.9%; Pred. No. 2.9e-90;
Matches 348; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGACATATGAGGTCCCGCTGAGCTCTTGCGCTCTTGTGCTGCTGCGCTCCAGGTGCC 60
DB 9 atgacatagaggtcccgctcagctccttggtgctcctgctactctgctcgcaggtgcc 68
QY 61 AGATGTGACATCCAGATGAGCCAGTCTCCATCTTCCCTGCTGCTGCTGAGGGAGAGA 120
DB 69 agatgtgacatccagatgagccagctccatctcctctgctcgtcgtcgtatgagagacaga 128
QY 121 GTGACCATCATCTTGACAGGCGCAAGTCAAGCATTAATTATTTAAATTGATACAGCAG 180
DB 129 gtgaccatcactctgcgggcaagtcagacattagcagctatataattgtatcagcag 188
QY 181 AACCCAGAAAGCTCTAGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 240
DB 189 aaaccagaaagctcttagctctgactctgactctgactctgactctgactctgactctg 248
QY 241 CCATCAAGGTTTACGCGCACTGATCTGGAGACAGATTTCATCTGCAAGCTGAGGCTG 300
DB 249 ccatacaggtcagtgagtcagtgatctggtgacagattcactcctcaccatcagcagctg 308
QY 301 CACCTGAGAGATTTTGGCACTTATTACTGCTCTACAGGTTTATAGTACCTCGAGCTTC 360
DB 309 caacctgaagatttgcacacttactactcacaagagtlactacagtlaccccgctacacttt 368
QY 361 GGCCAAAGGACCAAGTGGAAT 383
DB 369 ggcacagggacacaaagctgagat 391

RESULT 13
US-09-939-397-2087
Sequence 2087, Application US/09939397
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-765
CURRENT APPLICATION NUMBER: US/09/939,397
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/289,768
NUMBER OF SEQ ID NOS: 39996
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2087
LENGTH: 391
TYPE: DNA
ORGANISM: Homo sapiens
US-09-939-397-2087

Query Match 84.5%; Score 327; DB 35; Length 391;
Best Local Similarity 90.9%; Pred. No. 2.9e-90;
Matches 348; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGACATGAGGTCCCGCTGAGCTCTTGCGCTCTTGTGCTGCTGCGCTCCAGGTGCC 60
DB 9 atgacatgaggtcccgctcagctccttggtgctcctgctactcgtgcaggtgcc 68
QY 61 AGATGTGACATCCAGATGAGCCAGTCTCCATCTTCCCTGCTGCTGCTGAGGGAGAGA 120
DB 69 agatgtgacatccagatgagccagctccatctcctctgctcgtcgtcgtatgagagacaga 128

QY 121 GTGACCATCATCTTGACAGGCGCAAGTCAAGCATTAATTATTTAAATTGATACAGCAG 180
DB 129 gtgaccatcactctgcgggcaagtcagacattagcagctatataattgtatcagcag 188
QY 181 AACCCAGAAAGCTCTAGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 240
DB 189 aaaccagaaagctcttagctctgactctgactctgactctgactctgactctgactctg 248
QY 241 CCATCAAGGTTTACGCGCACTGATCTGGAGACAGATTTCATCTGCAAGCTGAGGCTG 300
DB 249 ccatacaggtcagtgagtcagtgatctggtgacagattcactcctcaccatcagcagctg 308
QY 301 CACCTGAGAGATTTTGGCACTTATTACTGCTCTACAGGTTTATAGTACCTCGAGCTTC 360
DB 309 caacctgaagatttgcacacttactactcacaagagtlactacagtlaccccgctacacttt 368
QY 361 GGCCAAAGGACCAAGTGGAAT 383
DB 369 ggcacagggacacaaagctgagat 391

RESULT 14
US-09-665-486-816
Sequence 816, Application US/09665486
GENERAL INFORMATION:
APPLICANT: Hodgson, David M.
APPLICANT: Lincoln, Stephen E.
APPLICANT: Russo, Frank D.
APPLICANT: Spiro, Peter A.
APPLICANT: Banville, Steve C.
APPLICANT: Bratcher, Shawn R.
APPLICANT: Dufour, Gerard E.
APPLICANT: Cohen, Howard J.
APPLICANT: Rosen, Bruce H.
APPLICANT: Shah, Purvi
APPLICANT: Chalup, Michael S.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Jones, Anissa L.
APPLICANT: Yu, Jimmy Y.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Panzer, Scott R.
APPLICANT: Roseberry, Ann M.
APPLICANT: Wright, Rachel J.
APPLICANT: Chen, Wensheng
APPLICANT: Liu, Tommy F.
APPLICANT: Yap, Pierre E.
APPLICANT: Stockdreher, Theresa K.
APPLICANT: Amshay, Stefan
APPLICANT: Bong, Willy T.
TITLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES
FILE REFERENCE: PT-0076 US
CURRENT APPLICATION NUMBER: US/09/665,486
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/156,297
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 60/156,624
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/156,625
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: 60/168,599
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/168,197
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/168,614
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/168,611
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/168,613
PRIOR FILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 958
SOFTWARE: PERL Program
SEQ ID NO 816
LENGTH: 549

```

: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 996142.1.dec
: NAME/KEY: unsure
: LOCATION: 488
: OTHER INFORMATION: a, t, c, g, or other
US-09-665-486-816

```

```

Query Match      84.3%; Score 326.2; DB 26; Length 549;
Best Local Similarity 90.2%; Pred. No. 5.9e-90;
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```

```

QY 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTGCTGCCAGGTGCC 60
   |||||||
Db 20 atgacatgaggggtcccgctcagctcctgggtcctcctgctcctcctcaggtgccc 79
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATGTAGGGGACAGA 120
   |||||||
Db 80 agctgtgccatccagatgacccagctccatccctcctgctcctgcatctgtagagacaga 139
QY 121 GTACCATCACTTGCAGGGCAAGTCAGACATTAAGTATTATTTAAATGGTATCAGCAG 180
   |||||||
Db 140 gtccatcaacttgcagggcagtcagacagctgtgaaatgattaggtgtatcagctg 199
QY 181 AAACGAGAAAGCTCCTTAAGCTCCTGATCTATGTGCATCCAGTTGCAAGTGGGCTC 240
   |||||||
Db 200 aaacgaggaagcccttaagctcctgctcctgctcctgcatccacaggtacacacggggtc 259
QY 241 CCATCAAGGTTCAGCGGACGTGATCTGGGACAGAGTTCACTTCACCGTCAGACGCTG 300
   |||||||
Db 260 ccatacaaggttcagcgagtgagatctgycacagattacacctccacatcagagctg 319
QY 301 CAGCCTGAGATTGCGACTTATTACTGTCTACAGGTTTATAGCCCTCGAGCGTTC 360
   |||||||
Db 320 cagcctgaagacttgcactattactgtctgcaagattacagttacccctcgagctg 379
QY 361 GCCCAAGGACCAAGGTGGAATCAA 387
   |||||||
Db 380 ggcacaaggaccaaagctgagatcaaa 406

```

```

RESULT 15
US-60-168-599-218
: Sequence 218, Application US/60168599
: GENERAL INFORMATION:
: APPLICANT: Hodgson, David M.
: APPLICANT: Lincoln, Stephen E.
: APPLICANT: Russo, Frank D.
: APPLICANT: Spito, Peter A.
: APPLICANT: Banville, Steve C.
: APPLICANT: Bratcher, Shawn R.
: APPLICANT: Dufour, Gerard E.
: APPLICANT: Cohen, Howard J.
: APPLICANT: Rosen, Bruce
: APPLICANT: Shah, Puri V.
: APPLICANT: Chalup, Michael S.
: APPLICANT: Hillman, Jennifer L.
: TITLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES
: FILE REFERENCE: PT-0099 P
: CURRENT APPLICATION NUMBER: US/60/168, 599
: NUMBER OF SEQ ID NOS: 737
: SOFTWARE: PERL Program
: SEQ ID NO 218
: LENGTH: 549
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 996142.1

```

```

: FEATURE:
: NAME/KEY: unsure
: LOCATION: 488
: OTHER INFORMATION: a, t, c, g, or other
US-60-168-599-218

```

```

Query Match      84.3%; Score 326.2; DB 55; Length 549;
Best Local Similarity 90.2%; Pred. No. 5.9e-90;
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

```

```

QY 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTGCTGCCAGGTGCC 60
   |||||||
Db 20 atgacatgaggggtcccgctcagctcctgggtcctcctgctcctcctcaggtgccc 79
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGATGTAGGGGACAGA 120
   |||||||
Db 80 agctgtgccatccagatgacccagctccatccctcctgctcctgcatctgtagagacaga 139
QY 121 GTACCATCACTTGCAGGGCAAGTCAGACATTAAGTATTATTTAAATGGTATCAGCAG 180
   |||||||
Db 140 gtccatcaacttgcagggcagtcagacagctgtgaaatgattaggtgtatcagctg 199
QY 181 AAACGAGAAAGCTCCTTAAGCTCCTGATCTATGTGCATCCAGTTGCAAGTGGGCTC 240
   |||||||
Db 200 aaacgaggaagcccttaagctcctgctcctgctcctgcatccacaggtacacacggggtc 259
QY 241 CCATCAAGGTTCAGCGGACGTGATCTGGGACAGAGTTCACTTCACCGTCAGACGCTG 300
   |||||||
Db 260 ccatacaaggttcagcgagtgagatctgycacagattacacctccacatcagagctg 319
QY 301 CAGCCTGAGATTGCGACTTATTACTGTCTACAGGTTTATAGCCCTCGAGCGTTC 360
   |||||||
Db 320 cagcctgaagacttgcactattactgtctgcaagattacagttacccctcgagctg 379
QY 361 GCCCAAGGACCAAGGTGGAATCAA 387
   |||||||
Db 380 ggcacaaggaccaaagctgagatcaaa 406

```

```

Search completed: September 23, 2002, 19:47:27
Job time: 7022 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:58:47 : Search time 662.78 Seconds
(without alignments)
1881.788 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387
Sequence: 1 ATGGACATGAGGTCCTCCCGC.....GGACCAAGTGTGAATCAAA 387

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents, NA, New: *
1: /cgn2_6/ptodata/1/pna/US05_NEW_COMB.seq: *
2: /cgn2_6/ptodata/1/pna/US05_NEW_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	387	100.0	729	US-10-103-686-3	Sequence 3, Appl
2	342.2	88.4	729	US-10-216-484-125	Sequence 125, Appl
3	335.2	86.6	812	US-10-206-008-405	Sequence 405, App
4	327.8	84.7	974	US-10-206-008-192	Sequence 192, Appl
5	326.2	84.3	714	US-10-153-382-18	Sequence 18, Appl
6	323	83.5	728	US-10-040-244-15	Sequence 15, Appl
7	321.4	83.0	514	US-10-214-403-2025	Sequence 2025, Ap
8	321.4	83.0	537	US-10-214-403-186	Sequence 186, App
9	321.4	83.0	716	US-10-040-244-13	Sequence 29, Appl
10	318	82.2	936	US-09-831-805A-29	Sequence 29, Appl
11	316.6	81.8	817	US-09-831-805A-28	Sequence 28, Appl
12	316.4	81.8	917	US-09-831-805A-20	Sequence 20, Appl
13	311.8	80.6	698	US-10-040-244-11	Sequence 11, Appl
14	311.8	80.6	944	US-09-602-148A-48	Sequence 48, Appl
15	310	80.1	634	US-10-158-646-55	Sequence 55, Appl
16	309.8	80.1	402	US-10-158-646-56	Sequence 56, Appl
17	308.8	79.8	520	US-10-146-502-1210	Sequence 1210, Ap
18	308.4	79.7	378	US-10-175-525-55	Sequence 55, Appl
19	304.2	78.6	705	US-09-335-697B-16	Sequence 16, Appl
20	303.6	78.4	928	US-09-831-805A-32	Sequence 32, Appl
21	302	78.0	494	US-10-146-502-1811	Sequence 1811, Ap
22	300.4	77.6	918	US-10-206-008-111	Sequence 111, App
23	299	77.3	490	US-09-918-995-37859	Sequence 37859, A
24	299	77.3	819	US-10-158-646-65	Sequence 65, Appl
25	298.8	77.2	583	US-10-198-846-8365	Sequence 8365, Ap

26	295	76.2	576	7	US-10-175-525-65	Sequence 65, Appl
27	295	76.2	3123	7	US-10-175-525-101	Sequence 101, App
28	289.2	74.7	372	7	US-10-175-525-78	Sequence 78, Appl
29	287.8	74.4	916	5	US-09-831-805A-24	Sequence 24, Appl
30	287.4	74.3	463	7	US-10-146-502-2039	Sequence 2039, Ap
31	286.2	74.0	890	5	US-09-831-805A-31	Sequence 31, Appl
32	285	73.6	384	7	US-10-089-500-30	Sequence 30, Appl
33	284.8	73.6	454	1	PCT-US02-18947-1918	Sequence 1918, Ap
34	284.8	73.6	454	7	US-10-172-118-1918	Sequence 1918, Ap
35	283.4	73.2	384	7	US-10-089-500-39	Sequence 39, Appl
36	281.8	72.8	384	7	US-10-089-500-27	Sequence 27, Appl
37	281.8	72.8	384	7	US-10-089-500-33	Sequence 33, Appl
38	281.8	72.8	384	7	US-10-089-500-42	Sequence 42, Appl
39	280.4	72.5	853	7	US-10-158-646-68	Sequence 68, Appl
40	279.4	72.2	720	5	US-09-511-939-1	Sequence 1, Appl
41	279.4	72.2	720	5	US-09-968-561A-1	Sequence 1, Appl
42	279.2	72.1	369	5	US-09-918-995-7569	Sequence 7569, Ap
43	279	72.1	438	6	US-10-198-846-5398	Sequence 5398, A
44	278.8	72.0	614	5	US-09-919-002-12346	Sequence 12346, A
45	278.6	72.0	384	7	US-10-089-500-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-10-103-686-3
Sequence 3, Application US/10103686
GENERAL INFORMATION:
APPLICANT: REFE, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..387
FEATURE:
NAME/KEY: mat_peptide

LOCATION: 67..387
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-10-103-686-3

Query Match 100.0%; Score 387; DB 7; Length 387;
Best Local Similarity 100.0%; Pred. No. 3,6e-107;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTGACGCTCTGGGGCTCTCTGCTGGCCCGCAGTGC 60
DB 1 ATGGACATGAGGGTCCCGCTGACGCTCTGGGGCTCTCTGCTGGCCCGCAGTGC 60
QY 61 AGATGACATCCAGATGAGCCAGTCTCATCTTCCCTGCTGCATCTGAGGGAGACA 120
DB 61 AGATGACATCCAGATGAGCCAGTCTCATCTTCCCTGCTGCATCTGAGGGAGACA 120
QY 121 GTACACATCTCTGACAGGCACTGACAGACATTAGTATTATTAAATTTGATCAGCAG 180
DB 121 GTACACATCTCTGACAGGCACTGACAGACATTAGTATTATTAAATTTGATCAGCAG 180
QY 181 AACACGAGAAAGCTCCTAGCTCCTGATCTATGTCATCCAGTTTGGCAAGTGGGCTC 240
DB 181 AACACGAGAAAGCTCCTAGCTCCTGATCTATGTCATCCAGTTTGGCAAGTGGGCTC 240
QY 241 CCATCAAGGTTTACGCGGCACTGATCTGGACAGAGTTTCACTCTCACCCTGACAGCTG 300
DB 241 CCATCAAGGTTTACGCGGCACTGATCTGGGACAGAGTTTCACTCTCACCCTGACAGCTG 300
QY 301 CAGCCTGAAGATTTTGGCAGATTATCTGCTCTCAGGTTTATAGTACCCTGGAGCTTC 360
DB 301 CAGCCTGAAGATTTTGGCAGATTATCTGCTCTCAGGTTTATAGTACCCTGGAGCTTC 360
QY 361 GGCCAAGGACCAAGGTGGAATCAAA 387
DB 361 GGCCAAGGACCAAGGTGGAATCAAA 387

RESULT 2

US-10-216-484-125
Sequence 125, Application US/10216484
GENERAL INFORMATION:
APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Pas Antibodies
FILE REFERENCE: 980126CTP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 125
LENGTH: 729
TYPE: DNA
ORGANISM: Homo sapiens
US-10-216-484-125

Query Match 88.4%; Score 342.2; DB 6; Length 729;
Best Local Similarity 92.8%; Pred. No. 1,6e-93;
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTGACGCTCTGGGGCTCTCTGCTGGCCCGCAGTGC 60
DB 7 ATGGACATGAGGGTCCCGCTGACGCTCTGGGGCTCTCTGCTGGCCCGCAGTGC 66
QY 61 AGATGACATCCAGATGAGCCAGTCTCATCTTCCCTGCTGCATCTGAGGGAGACA 120
DB 61 AGATGACATCCAGATGAGCCAGTCTCATCTTCCCTGCTGCATCTGAGGGAGACA 120

DB 67 agatgtacacaccagatgaccacgtctccatccctctgtctgcatctgtaggagacaga 126
QY 121 GTACACATCTCTGACAGGCACTGACAGATAGTATTATTAAATTTGATCAGCAG 180
DB 127 gtacacatcttgcggaagatcagatcattagcagcatttaattgtagtcagcag 186
QY 181 AACACGAGAAAGCTCCTAGCTCCTGATCTATGTCATCCAGTTTGGCAAGTGGGCTC 240
DB 187 aaacacaggaagcccttaagctctcgtatctatgtcgtcagatctgcaagtgaggc 246
QY 241 CCATCAAGGTTTACGCGGCACTGATCTGGACAGAGTTTCACTCTCACCCTGACAGCTG 300
DB 247 ccatcaaggttcagtgagtgatctggaacagatctcaccatcagcagctc 306
QY 301 CAGCCTGAAGATTTTGGCAGATTATCTGCTCTCAGGTTTATAGTACCCTGGAGCTTC 360
DB 307 caacctgaagatcttgaaactactcagcaacagagttacagttacctcgaaagcttc 366
QY 361 GGCCAAGGACCAAGGTGGAATCAAA 387
DB 367 ggcacaaggagcacaagtggaatcaaa 393

RESULT 3

US-10-206-008-405
Sequence 405, Application US/10206008
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT253CJN
CURRENT APPLICATION NUMBER: US/10/206,008
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 09/760,479
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/216,647
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,270
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/234,274
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/234,223
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/228,924

;;
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/224,518
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,369
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/224,519
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,964
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/236,327
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/225,268
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/236,368
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/251,856
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/251,868
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/229,344
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: 60/229,343
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,287
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,513
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/231,413
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PRIOR APPLICATION NUMBER: 60/229,509
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PRIOR APPLICATION NUMBER: 60/236,367
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/237,039
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,038
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/236,370
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/236,802
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,037
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,210
PRIOR FILING DATE: 2000-11-17

;;
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759
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PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218
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PRIOR FILING DATE: 2000-09-08
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PRIOR APPLICATION NUMBER: 60/232,399
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065

Query Match      86.6%; Score 335.2; DB 6; Length 812;
Best Local Similarity 90.2%; Pred. No. 2,2e-91;
Matches 349; Conservative 7; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGACATGAGGGTCCCGCTCAGCTCTCTGGGCTCTTCTGCTCTGGCTCCAGGGTCC 60
Db 41 atgacatgaggggtcccgctcagctctctgggctcttctgctctggctccaggggtcc 100
QY 61 AGATGTACATTCAGATGACCCAGCTTCATCTCCCTGCTGCTGATGAGGAGAGA 120
Db 101 agatgtacatgacatgacccagcttcattctccctgctgcatctgtagagagaca 160
QY 121 GTACACATCTTCAGAGGCAAGTACAGACATTAGTATTATTTAAATGGTATACAGAC 180
Db 161 gtacacatcttccagagcagagtcacatcaccatcctgctgcatctgtagagagaca 220
QY 181 AATCCAGAAAGCTCTTAAGCTCTATCTATGTTCATTCAGATTCGAAAGGGGCTC 240
Db 221 aatccagaaagcctcttaagctctatctatgtttcatcttcacacttgcagaaagggtc 280
QY 241 CCATCAAGGTTTCAGCGGAGTGTGATGATGGAGAGTTCACTCTCAGCGAGGCTG 300
Db 281 ccataaggttcagtgctgagtgatgagtgagagagattcactccacacatcagtgctg 340
QY 301 CAGCCTAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCTCGAGCTTC 360
Db 341 cagcctaagatttgggacttattactgtctacaggtttatagttaccctcgagcttc 400
QY 361 GGCCAAGGAGCAAGGTGAATCAA 387
Db 401 ggccaaggagcaaggtgaaatcaaa 427

RESULT 4
US-10-206-008-192
; Sequence 192, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253C1N
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
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; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
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; PRIOR APPLICATION NUMBER: 60/225,270
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; PRIOR APPLICATION NUMBER: 60/251,869
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; PRIOR FILING DATE: 2000-10-20
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; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
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; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
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; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
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PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/240,960
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/239,937
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/246,532
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/249,216
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PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
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PRIOR APPLICATION NUMBER: 60/231,244
PRIOR FILING DATE: 2000-09-08

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PRIOR FILING DATE: 2000-09-14
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PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
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PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065

Query Match 84.7% Score 327.8; DB 6; Length 974;
Best Local Similarity 90.4%; Pred. No. 4,1e-89;
Matches 350; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

OY 1 ATGACATGAGGCTCCCGCTCAGCTCCTGCGGCTCCTGCTGCGCTCAGGAGGCGG 60
|||||
DB 16 atggacatgaggtcccgctcagctcctggtggtctctgctacccgctcagagtgcc 75
|||||
OY 61 AGATGTGACATTCAGATGACCCAGTCCATCTTCCTGCTGCTGATGAGGAGAGA 120
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DB 76 agatgtgacatccagatgacccagctccatccctctgctgctgagagacaga 135
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OY 121 GTCACCATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
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DB 136 gtccacatccctgctgagagagagagagagagagagagagagagagagagag 195
|||||
OY 181 AACACGAGAAAGCTCTAGGCTCTGATCTGATCTGATCTGATCTGATCTGATCTG 240
|||||
DB 196 aaacacaggaagccctcagagctcctgctgctgctgctgctgctgctgctgctg 255
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OY 241 CCATCAAGTTTCAGGCGCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
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DB 256 ccacacaggtcagtgagagagagagagagagagagagagagagagagagag 315
|||||
OY 301 CAGCTGAAGTTTGGGAGCTTATTACTGCTACAGGTTTATACCTCGGAGCTTC 360
|||||
DB 316 caactgaagatttggacttattacttacttacttacttacttacttacttactt 375
|||||
OY 361 GGCCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387
|||||
DB 376 ggcacagggagacacagctgagagatcaaa 402
|||||

RESULT 5
US-10-153-382-18
Sequence 18, Application US/10153382
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 714
TYPE: DNA

ORGANISM: Homo sapiens
US-10-153-382-18

Query Match 84.3%: Score 326.2; DB 7: Length 714;
Best Local Similarity 90.2%: Pred. No. 1.2e-88;
Matches 34; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGACATGAGGCTCCCGCTCAGCTCTGCGGGCTCTTCTGCTGTGCTCCAGAGTGC 60
Db 1 atgacatgagggctcccgctcagctctctgggctctctgctctctctgctccgaggtgc 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGAGACA 120
Db 61 agatgtgacatccagatgacccagtcctccatctccctgctgcatctgtatggagaca 120
QY 121 GTCAACATCACTTCAGAGGCAAGTACAGCATATGATATTAATTTAGTATCAGACAG 180
Db 121 gtcaacatcacttcagagggcaagtcagacatataagctatctagatgtatcagacag 180
QY 121 gtcaacatcacttcgagggcaagtcagacatataagctatctagatgtatcagacag 180
Db 121 gtcaacatcacttcgagggcaagtcagacatataagctatctagatgtatcagacag 180
QY 181 AACCCAGGAAAGCTCCTTAAGCTCCTGATCTATGTGCATCCAGTTTGCAAGTGGGCTC 240
Db 181 aaccaggaagagcccttaactctgctatgctgcatcagtttgcaagtgaggctc 240
QY 241 CCATCAAGGCTCAGCGCAGTGGATCTGAGACAGATTCACTCTCACCCTAGACAGCTG 300
Db 241 ccatacaggctcagcgctagtgatgagacagattcactctaccatcagacagctg 300
QY 301 CAGCCTGAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGAGTTC 360
Db 301 caactgagagtttggcacttactactgctacaagctatcagtaactcactc 360
QY 361 GGCCAAGGACCAAGTGGAAATCAA 387
Db 361 ggcctggagcaagtggaatcaaa 387

RESULT 6
US-10-040-244-15
Sequence 15, Application US/10040244
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: FORCE, WALKER F.
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
FILE REFERENCE: 021286/0272501
CURRENT APPLICATION NUMBER: US/10/040,244
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/200,601
PRIOR FILING DATE: 2000-4-28
PRIOR APPLICATION NUMBER: PCT/US01/13672
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/844,684
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 15
LENGTH: 728
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-244-15

Query Match 83.5%: Score 323; DB 7: Length 728;
Best Local Similarity 89.7%: Pred. No. 1.1e-87;
Matches 34; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 ATGACATGAGGCTCCCGCTCAGCTCTGCGGGCTCTTCTGCTGTGCTCCAGAGTGC 60
Db 59 atgacatgagggctcccgctcagctctctgggctctctgctctctgctccgaggtgc 118
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGAGACA 120

Db 119 agatgtgacatccagatgacccagctcctcactctctgctggtatgtatgagagaca 178
QY 121 GTCAACATCACTTCAGAGGCAAGTACAGCATATGATATTAATTTAGTATCAGACAG 180
Db 121 gtcaacatcacttcagagggcaagtcagacatataagctatctagatgtatcagacag 238
QY 181 AACCCAGGAAAGCTCCTTAAGCTCCTGATCTATGTGCATCCAGTTTGCAAGTGGGCTC 240
Db 239 aaccaggaagagcccttaactctctgctatgctgcatcagtttgcaagtgaggctc 298
QY 241 CCATCAAGGCTCAGCGCAGTGGATCTGAGACAGATTCACTCTCACCCTAGACAGCTG 300
Db 299 ccatacaggctcagcgagtgatgagacagattcactcaccatcagacagctg 358
QY 301 CAGCCTGAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGAGTTC 360
Db 359 cagctgagagtttggcacttactatgttacaagctagcagttccctcgagactc 418
QY 361 GGCCAAGGACCAAGTGGAAATCAA 387
Db 419 ggcgaaggaagagtgagatcaaa 445

RESULT 7
US-10-214-403-2025
Sequence 2025, Application US/10214403
GENERAL INFORMATION:
APPLICANT: Jiang, Yuguo
APPLICANT: Chenault, Ruth A.
APPLICANT: Xu, Jiangchun
APPLICANT: Indrias, Carol Yoseph
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Carter, Darick
APPLICANT: Fanger, Gary R.
APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margalita
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.563CI
CURRENT APPLICATION NUMBER: US/10/214,403
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 3420
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2025
LENGTH: 514
TYPE: DNA
ORGANISM: Homo sapiens
US-10-214-403-2025

Query Match 83.0%: Score 321.4; DB 6: Length 514;
Best Local Similarity 89.4%: Pred. No. 3e-87;
Matches 34; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 ATGACATGAGGCTCCCGCTCAGCTCTGCGGGCTCTTCTGCTGTGCTCCAGAGTGC 60
Db 12 atgacatgagggctcccgctcagctctctgggctctctgctctctgctccgagaca 71
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGAGACA 120
Db 72 agatgtgacatccagatgacccagtcctccatctccctgctgcatctgtagagagaca 131
QY 121 GTCAACATCACTTCAGAGGCAAGTACAGCATATGATATTAATTTAGTATCAGACAG 180
Db 132 gtcaacatcacttcagagggcaagtcagacatataagctatctagatgtatcagacag 191
QY 181 AACCCAGGAAAGCTCCTTAAGCTCCTGATCTATGTGCATCCAGTTTGCAAGTGGGCTC 240
Db 192 aaccaggaagagctccttaagctcctcactatgctgcatcagtttgcaacttgcaatctgaggtc 251

QY 241 CCATCAAGCTTCAGCGGCACTGCATCTGGACAGAGTTCACTCTACCCGTCCAGACGCTTG 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 252 ccatctgcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 311
QY 301 CAGCGTGAAGATTGTCGACTTATCTGCTCTACAGAGTTATAGTACCCTCGAGAGCTTC 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 312 cagccggaagatgctgcaactatcttcgcaaaaalataacagtcgccccggagagcttc 371
QY 361 GGCCAAAGGACCAAGGTGAATCAAA 387
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 372 ggcgaagggaccaagtgatgacatcaaa 398
RESULT 8
US-10-214-403-186/C
; Sequence 186, Application US/10214403
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Chenuault, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Joseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darick
; APPLICANT: Ronger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margareta
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563c1
; CURRENT APPLICATION NUMBER: US/10/214,403
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 3420
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 529
; OTHER INFORMATION: n = A,T,C or G
US-10-214-403-186
Query Match 83.0%; Score 321.4; DB 6; Length 537;
Best Local Similarity 89.4%; Pred. No. 3e-87;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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Db 503 ATGGACATGAGGGTCCCGCTCAGACTCTGGGGCTCCTTCTGCTCTGCTGCCAGGTGCC 444
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGAGAGA 120
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Db 443 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGAGAGA 384
QY 121 GTCAACATCACTTGCAGGGGCAAGTCAAGACATTAGTATTAAATTGGTATACAGCAG 180
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Db 383 GTCAACATCACTTGCAGGGGCAAGTCAAGACATTAGTATTAAATTGGTATACAGCAG 324
QY 181 AAACGAGAAAGCTCCTTAAGCTCCTGATCTATGTTGCATCCAGATTGCAAAAGTGGGTC 240
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QY 241 CCATCAAGCTTCAGCGGCACTGCATCTGGAGAGAGTTCACTCTACCCGTCCAGAGCTTG 300
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Db 263 CCATCTGCTGTCAGTGCAGTGTGAGACACATTTCACCTCCACATCGCGAGCTG 204
QY 301 CAGCGTGAAGATTGTCGACTTATCTGCTCTACAGAGTTATAGTACCCTCGAGAGCTTC 360
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Db 203 CAGCGTGAAGATTGTCGACTTATCTGCTCTACAGAGTTATAGTACCCTCGAGAGCTTC 144

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Db 143 GGCCAAAGGACCAAGGTGAATCAAA 117
RESULT 9
US-10-040-244-13
; Sequence 13, Application US/10040244
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIEDU
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentln Ver. 3.0
; SEQ ID NO 13
; LENGTH: 716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-13
Query Match 83.0%; Score 321.4; DB 7; Length 716;
Best Local Similarity 89.4%; Pred. No. 3.3e-87;
Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
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Db 47 atgacatgaggggtcccgctcagctcctggtggtcctcctgctcctgctcctgctcctgctcctgctcct 106
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QY 181 AAACGAGAAAGCTCCTTAAGCTCCTGATCTATGTTGCATCCAGATTGCAAAAGTGGGTC 240
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Db 227 aaacgaagaaagcccttaagctcctgctcctgctcctgctcctgctcctgctcctgctcctgctcctgctcctgctcct 286
QY 241 CCATCAAGCTTCAGCGGCACTGCATCTGGAGAGAGTTCACTCTACCCGTCCAGAGCTTG 300
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Db 287 ccatcaaggttcagcgagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 346
QY 301 CAGCGTGAAGATTGTCGACTTATCTGCTCTACAGAGTTATAGTACCCTCGAGAGCTTC 360
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Db 347 cagcgtgaagatttgcgaacttactatgtcgaacagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 406
QY 361 GGCCAAAGGACCAAGGTGAATCAAA 387
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Db 407 ggcgaagggaccaagtgatgacatcaaa 433

RESULT 10
US-09-831-805A-29
; Sequence 29, Application US/09831805A
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom

```

:   APPLICANT : YANG, Junming
:   TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
:   FILE REFERENCE: PF-0643 PCT
:   CURRENT APPLICATION NUMBER: US/09/831.805A
:   PRIOR FILING DATE: 2002-08-26
:   PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/113,635; 60/128,194
:   PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07
:   NUMBER OF SEQ ID NOS: 38
:   SOFTWARE: PERL Program
:   SEQ ID NO 28
:   LENGTH: 817
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   NAME/KEY: misc-feature
:   OTHER INFORMATION: Incyte ID NO: 2851053CBI
:   US-09-831-805A-28

Query Match      81.8%; Score 316.6; DB 5; Length 817;
Best Local Similarity 88.6%; Pred No. 9,7e-86;
Matches 343; Conservative 0; Mismatches 44; Indels 0; Gaps 0

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Matches 352; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
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QY	121	GTCCACCATCAGTTCGACGGGACAGTTCAGGACATTAGGTATTTAAATTGGTATCAGCAG	180
Db	131	gtccacatcaactctcgcgagcagcaatcatagcaattatattagccgttcttcagcag	190
QY	181	AAACACGAAAGAAGTCTCTAAGCTCCTGATGCTGATGTTGATCCAGTTTGGCAAGTGGGGTC	240
Db	191	aaacacaggaagaaagcccttaagtcctccatgatatacatcacagtttggaaagtggggttc	250
QY	241	CCATCAAGAGTTCCAGCGGCACTGATCGATCGGAGACAGTTCAGTCCGTCAGCAGCCTG	300
Db	251	ccatcaaaagtttcagcgcagttgatactcggagacatgttccatctccatcacaaagccgtc	310
QY	301	CAGCCTCAAGAATTTTGGGACTTATTACTGTCTACAGGTTTAAAGTACCCCTCGAGCTTC	360
Db	311	cagcctcaagaagtttggaaacttattactgcacaacagatcatagttatcctcttactttc	370
QY	361	GGCCAAGGAGACCAAGGTGGAATCAAA	387
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RESULT 12
 US-09-831-R05A-20
 ; Sequence 20, Application US/09831805A
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE PHARMACEUTICALS, INC.

RESULT 12
US-09-831-805A-20
Sequence 20. Application US/09831805A
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: YUE, Henry
APPLICANT: TANG, Y.-Tom
APPLICANT: CORLEY, Neil C.
APPLICANT: GUEGLER, Karl J.
APPLICANT: GORGONE, Gina A.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LU, Dyung Anna M.
APPLICANT: LAL, Preeti
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: YANG, Junming
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0643 PCT
CURRENT APPLICATION NUMBER: US/09/831,805A
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/113,635; 60/128,194
PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 18:00:51 ; Search time 110.65 Seconds
(without alignments)
859,107 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGGACATGAGGCTCCCCGC.....GGACCAAGTGGAATCAAA 387

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

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6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	387	100.0	387	3	US-08-803-085-3
2	318.2	82.2	388	4	US-09-042-353-358
3	318.2	82.2	388	4	US-08-758-417A-206
4	316.6	81.8	1066	1	US-08-157-101A-4
5	308.6	79.7	387	1	US-08-217-918-1
6	307.7	79.3	439	4	US-09-042-353-360
7	307.7	79.3	439	4	US-08-758-417A-208
8	304.2	78.6	705	1	US-08-488-376-16
9	304.2	78.6	705	2	US-08-634-223-16
10	304.2	78.6	705	2	US-08-634-224-16
11	304.2	78.6	705	2	US-08-634-400-16
12	304.2	78.6	705	2	US-08-635-878-16
13	304.2	78.6	705	2	US-08-770-057-16
14	304.2	78.6	705	4	US-09-335-697B-16
15	302	78.0	420	4	US-09-042-353-420
16	302	78.0	420	4	US-08-758-417A-220
17	302	78.0	3819	4	US-09-042-353-393
18	302	78.0	3819	4	US-08-758-417A-243
19	297.4	76.8	390	2	US-08-646-367-2
20	296.2	76.5	384	1	US-08-259-372A-13
21	296.2	76.5	384	1	US-08-468-671-13
22	279.4	72.2	324	2	US-08-378-939-23
23	278.2	71.9	708	1	US-08-488-376-18
24	278.2	71.9	708	2	US-08-634-223-18
25	278.2	71.9	708	2	US-08-634-224-18
26	278.2	71.9	708	2	US-08-634-400-18
27	278.2	71.9	708	2	US-08-635-878-18

28	278.2	71.9	708	2	US-08-770-057-18	Sequence 18, Appl
29	278.2	71.9	708	2	US-09-335-697B-18	Sequence 18, Appl
30	273.8	70.7	381	2	US-08-621-751A-5	Sequence 5, Appl
31	269.6	69.7	321	4	US-09-240-274-102	Sequence 102, Appl
32	269.6	69.7	321	4	US-09-240-274-218	Sequence 218, Appl
33	269.6	69.7	321	4	US-09-240-274-221	Sequence 221, Appl
34	269.6	69.7	321	4	US-09-240-274-222	Sequence 222, Appl
35	269.6	69.7	321	4	US-08-346-561-70	Sequence 70, Appl
36	268.6	69.4	401	1	US-08-472-788A-47	Sequence 47, Appl
37	268.6	69.4	401	1	US-08-472-788A-47	Sequence 47, Appl
38	268.6	69.4	401	1	US-08-472-788A-47	Sequence 47, Appl
39	268.6	69.4	401	2	US-08-082-842A-47	Sequence 47, Appl
40	268.6	69.3	321	4	US-09-240-274-105	Sequence 105, Appl
41	266.4	68.8	321	4	US-09-240-274-107	Sequence 107, Appl
42	266.4	68.8	321	4	US-09-240-274-216	Sequence 216, Appl
43	265	68.5	324	2	US-08-378-939-17	Sequence 17, Appl
44	264.8	68.4	321	4	US-09-240-274-98	Sequence 98, Appl
45	264.8	68.4	321	4	US-09-240-274-104	Sequence 104, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-3
; Sequence 3, Application US/08803085
; Patent No. 601138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHEIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; NAME/KEY: CDS
; LOCATION: 1..387
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 67..387
; US-08-803-085-3

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Query Match Similarity      100.0%; Score 387; DB 3; Length 387;
Best Local Similarity      100.0%; Pred. No. 8,4e-113;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1  ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCTCTGCTGCGTCCAGGTGCC 60
OY      61  AGATGTGACATCCACATGACCAAGTCCTCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
DB      61  AGATGTGACATCCACATGACCAAGTCCTCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
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DB      121  GTCACATCTACTTGGAGGGCAAGTCAGGACATTTAGTATTTAAATGGTATGACAG 180
OY      181  AAACGAGGAAAAAGCTCTTAAGCTCTGATCTATGTGTCATCCAGTTTGGCAAGTGGGTC 240
DB      181  AAACGAGGAAAAAGCTCTTAAGCTCTGATCTATGTGTCATCCAGTTTGGCAAGTGGGTC 240
OY      241  CCATCAAGTTTCAGGGGCGAGTGGATCTGGGACAGAGTTCACTCTACCGTCAGCAGCTTG 300
DB      241  CCATCAAGTTTCAGGGGCGAGTGGATCTGGGACAGAGTTCACTCTACCGTCAGCAGCTTG 300
OY      301  CAGCCTGAAGATTTTGGCGATTTACTGTCTACAGGTTTATAGTACCCTGGAGCTTC 360
DB      301  CAGCCTGAAGATTTTGGCGATTTACTGTCTACAGGTTTATAGTACCCTGGAGCTTC 360
OY      361  GCCCAAGGACCAAGGTGGAATCAA 387
DB      361  GCCCAAGGACCAAGGTGGAATCAA 387

RESULT      2
US-09-042-353-358
: Sequence 358, Application US/09042353
: Patent No. 6255458
: GENERAL INFORMATION:
: APPLICANT: Lonberg, Nils
: APPLICANT: Kay, Robert M.
: TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
: TITLE OF INVENTION: Producing Heterologous Antibodies
: NUMBER OF SEQUENCES: 421
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/042.353
: FILING DATE: 13-MAR-1998
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/810,279
: FILING DATE: 17-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/853,408
: FILING DATE: 18-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/904,068
: FILING DATE: 23-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/990,860
: FILING DATE: 16-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/053,131

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Db 241 CCATCAAGTTGACGGGAGTGTGACAGATTTCACTCACCATCAGCAGCTG 300
QY 301 CAGCCTGAGATTTTGGAGTTTACTGTCTACAGGTTTATAGTACCCTCGAGCTTC 360
Db 301 CAGCCTGAGATTTTGGAGTTTACTGTCTACAGGTTTATAGTACCCTCGAGCTTC 360
QY 361 GGGCAAGGACCAAGGTGAAATCAA 387
Db 361 GGGCAAGGACCAAGGTGAAATCAA 387

RESULT 3
US-08-758-417A-206
; Sequence 206, Application US/08758417A
; Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 206:

US-08-758-417A-206
Query Match 82.2%; Score 318.2; DB 4; Length 388;
Best Local Similarity 88.9%; Pred. No. 4e-91;
Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 1 ATGACATGAGGGTCCCGCTCAGCTCCTGCGGCTCTTGTGCTGCTCCAGGTGC 60
Db 1 ATGACATGATGGTCCCGCTCAGCTCCTGCGGCTCTTGTGCTGCTCCAGGTTC 60
QY 61 AGATGTGACATCCAGATGACCCAGTCTTCATCTTCCCTGTCTGATCTGTAGGGAGAGA 120
Db 61 AGATGACATCCAGATGACCCAGTCTTCATCTTCCCTGTCTGATCTGTAGGGAGAGA 120
QY 121 GTCACATCACTTCGAGGAGCAGACATTTAGTATTAAATTTGGTATCAGCAG 180
Db 121 GTCACATCACTTCGAGGAGCAGACATTTAGTATTAAATTTGGTATCAGCAG 180
QY 181 AAACCAAGAAAGCTCCTAAGCTCTGATCTATGTATGATGATCAAGTTCAGAAAGTGGGCTC 240
Db 181 AAACCAAGAAAGCTCCTAAGCTCTGATCTATGTATGATGATCAAGTTCAGAAAGTGGGCTC 240
QY 241 CCATCAAGTTGACGGGAGTGTGACAGATTTCACTCACCATCAGCAGCTG 300
Db 241 CCATCAAGTTGACGGGAGTGTGACAGATTTCACTCACCATCAGCAGCTG 300
QY 301 CAGCCTGAGATTTTGGAGTTTACTGTCTACAGGTTTATAGTACCCTCGAGCTTC 360
Db 301 CAGCCTGAGATTTTGGAGTTTACTGTCTACAGGTTTATAGTACCCTCGAGCTTC 360
QY 361 GGGCAAGGACCAAGGTGAAATCAA 387
Db 361 GGGCAAGGACCAAGGTGAAATCAA 387

RESULT 4
US-08-157-101A-4
; Sequence 4, Application US/08157101A
; Patent No. 5808032
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: MATSUKURA, SHIGEKAZU
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENDI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARIANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437/204199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUCH

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1066 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-157-101A-4

Query Match 81.8%; Score 316.6; DB 1; Length 1066;
Best Local Similarity 88.6%; Pred. No. 1,9e-90;
Matches 343; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 60
DB 33 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 92
QY 61 AGATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 120
DB 93 AGGTGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 152
QY 121 GTACCATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 180
DB 153 GTACCATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 212
QY 181 AACACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATTTAAATGGTATCAGCAG 240
DB 213 AACACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATTTAAATGGTATCAGCAG 272
QY 241 CCATCAAGGTTTACAGGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300
DB 273 CCATCAAGGTTTACAGGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 332
QY 301 CAGCCTGAAGATTTTGGACCTTATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 360
DB 333 CAGCCTGAAGATTTTGGACCTTATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 392
QY 361 GGCACAGGACCAAGGTGGAATCAAA 387
DB 393 GGCACAGGACCAAGGTGGAATCAAA 419

RESULT 5
US-08-217-918-1

; Sequence 1, Application US/08217918
; Patent No. 5506132
; GENERAL INFORMATION:
; APPLICANT: LAKE, PHILIP
; APPLICANT: OSTERBERG, LARS
; TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
; TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,918
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..387
US-08-217-918-1

Query Match 79.7%; Score 308.6; DB 1; Length 387;
Best Local Similarity 87.3%; Pred. No. 4.2e-88;
Matches 338; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 60
DB 1 ATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 60
QY 61 AGATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 120
DB 61 AGATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 120
QY 121 GTACCATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 180
DB 121 GTACCATGACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTTGTGCTGCTGCCAGGTGCC 180
QY 181 AACACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATTTAAATGGTATCAGCAG 240
DB 181 AACACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATTTAAATGGTATCAGCAG 240
QY 241 CCATCAAGGTTTACAGGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300
DB 241 CCATCAAGGTTTACAGGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 300
QY 301 CAGCCTGAAGATTTTGGACCTTATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 360
DB 301 CAGCCTGAAGATTTTGGACCTTATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 360
QY 361 GGCACAGGACCAAGGTGGAATCAAA 387
DB 361 GGCACAGGACCAAGGTGGAATCAAA 387

RESULT 6

US-09-042-353-360
; Sequence 360, Application US/09042353
; Patent No. 6255458

; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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1  APPLICATION NUMBER: US/09/042,353
2  FILING DATE: 13-MAR-1998
3  CLASSIFICATION: 800
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: US 07/810,279
6  FILING DATE: 17-DEC-1991
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: US 07/853,408
9  FILING DATE: 18-MAR-1992
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 07/904,068
12 FILING DATE: 23-JUN-1992
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/990,860
15 FILING DATE: 16-DEC-1992
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/053,131
18 FILING DATE: 26-APR-1993
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/096,762
21 FILING DATE: 22-JUL-1993
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/155,301
24 FILING DATE: 18-NOV-1993
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/161,739
27 FILING DATE: 03-DEC-1993
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/165,699
30 FILING DATE: 10-DEC-1993
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/209,741
33 FILING DATE: 09-MAR-1994
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 08/352,322
36 FILING DATE: 07-DEC-1994
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 08/544,404
39 FILING DATE: 10-OCT-1995
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 08/728,463
42 FILING DATE: 10-OCT-1996
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: WO PCT/US96/16433
45 FILING DATE: 10-OCT-1996
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: US 08/758,417
48 FILING DATE: 02-DEC-1996
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: WO PCT/US97/21803
51 FILING DATE: 01-DEC-1997
52 ATTORNEY/AGENT INFORMATION:
53 NAME: Apple, Randolph T.
54 REGISTRATION NUMBER: 36,429
55 REFERENCE/DOCKET NUMBER: 014643-009040US
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: (415) 576-0200
58 TELEFAX: (415) 576-0200
59 INFORMATION FOR SEQ ID NO: 360:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 439 base pairs
62 TYPE: nucleic acid
63 STRANDEDNESS: single
64 TOPOLOGY: linear
65 MOLECULE TYPE: DNA
66 US-09-042-353-360

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Query Match	79.38;	Score 307;	DB 4;	Length 439;
Best Local Similarity	87.1%;	Pred. No. 1.4e-87;		
Matches 337;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0
1 ATGACATGAGGATCCCCGCTCAGCTCCTCGGGGCTCTTTCAGCTCTGAGCTCCCAAGGTGCC 60				

Db	1	ATGAGCATGGAGTTCCCCGTTTACAGTCTCCTGGGGGCTCCTGGCTGCTGTTCGCCAGGTGCC	60
QY	61	AGATGTACATCCAGATGATGACCCAGTCATCTTCCCTGTGTGATCTGTAGGGGACAGA	120
Db	61	AGATGTACATCCAGATGATGACCCAGTCATCTTCCCTGTGTGATCTGTAGGGGACAGA	120
QY	121	GTCCACATCACTTTCAGGGCAGGACAGACATAGTATTATTAAATTGTAATCAGACAG	180
Db	121	GTCCACATCACTTTCAGGGCAGGACAGGATTTAGCAGCTGGTTAGCCTGTATCAGCAG	180
QY	181	AAACCCAGAAAAGCTCCTTAAGCTTCGTATGTATGTTTCATCCAGTTTGCAAAGTGGGTC	240
Db	181	AAACCAAGAAAAGCCCTTAAGTCCCTGATCTATCTCATCCAGTTTGCAAAGTGGGTC	240
QY	241	CCATCAGGTTCCAGGGCAGTGGATCTGGGACAGAGTCACTCCACAGCCGACAGAGCTG	300
Db	241	CCATCAGGTTCCAGGGCAGTGGGACAGATTTCACTCCACATCAGCAGAGCTG	300
QY	301	CAGCCTCAAGATTTTGGACATTATTACTGTCTACAGGTTTATATACCCCTCGGACGTC	360
Db	301	CAGCCTCAAGATTTTGGACATTATTACTGCCACAGATATGATTTACCCGTACACTTTT	360
QY	361	GGCCCAAGGACCAAGTGTGAATATAA	387
Db	361	GGCCAGGGACCAAGCTGTGAATATAA	387

RESULT 7
 US-08-758-417A-208
 : Sequence 208, Application US/08/58417A
 : Patent No. 6300129
 :
 : GENERAL INFORMATION:
 : APPLICANT: Lomborg, Nils
 : Kay, Robert M.
 :
 : TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
 : Producing Heterologous Antipodotes
 :
 : NUMBER OF SEQUENCES: 417
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, Eighth Floor
 : CITY: San Francisco
 : STATE: California
 : COUNTRY: USA
 :
 : ZIP: 94111-3834
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/758,417A
 : FILING DATE: 02-Dec-1996
 :
 : CLASSIFICATION: <unknown>
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/728,463
 : FILING DATE: 10-OCT-1996
 : APPLICATION NUMBER: US 08/544,404
 : FILING DATE: 10-OCT-1995
 : APPLICATION NUMBER: US 08/352,322
 : FILING DATE: 07-DEC-1994
 : APPLICATION NUMBER: US 08/209,741
 : FILING DATE: 09-MAR-1994
 : APPLICATION NUMBER: US 08/165,699
 : FILING DATE: 10-DEC-1993
 : APPLICATION NUMBER: US 08/161,739
 : FILING DATE: 03-DEC-1993
 : APPLICATION NUMBER: US 08/155,301
 : FILING DATE: 18-NOV-1993
 : APPLICATION NUMBER: US 08/096,762
 : FILING DATE: 22-JUL-1993
 : APPLICATION NUMBER: US 08/053,131
 : FILING DATE: 26-APR-1993

Query Match	79.3%	Score 307;	DB 4;	Length 439;
Best Local Similarity	87.1%	Pred. No. 1.4e-87;		
Matches 337;	Conservative 0;	Mismatches 50;	Indels 0;	Gaps 0

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? COUNTRY: United States
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/488,376
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Teskin, Robin L.
? REGISTRATION NUMBER: 35,030
? REFERENCE/DOCKET NUMBER: 012712-150
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 836-6620
? TELEFAX: (703) 836-2021
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 705 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..705
? US-08-488-376-16

Query Match 78.6%, Score 304.2, DB 1: Length 705;
Best Local Similarity 87.4%, Pred. No. 1,3e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0.

QY 7 ATGAGGGTCCCGGCTGCACCTCCTGGGGGCTCCTTGTGCTGGCTCCAGAGTCCAGATGT 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGAGACCCTGCTGCACCTCCTGGGGGCTCCTGCTACTCTGGCTCCAGAGTCCAGATGT 60

QY 67 GACATCCAGATGACCCAGTCTTCATCTTCCCTGTCTGCATCTGTAGGGGACAGATCACC 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GACATCCAGATGACCCAGTCTTCATCTTCCCTGTCTGCATCTGTAGGGGACAGATCACC 120

QY 127 ATCACTTCAGAGGGCAGACGACATTAAGTATTTAAATTGGTATCAGCAAAACCA 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ATCACTTCAGAGGGCAGACGATTAAGTATTTAAATTGGTATCAGCAAAACCA 180

QY 187 GAAAAGCTCTTAAGCTTCGTATGTATGTGCATCCAGATTGGCAAAAGTGGGCTCCATCA 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GGGAAAGCCCTTAAGCTTCGTATGTATGTGCATCCAGATTGGCAAAAGTGGGCTCCGATCA 240

QY 247 AGGTTACAGCGCAGTGGATCTGGGACAGAGTTCACTCTACCGGTAGACGACCTGCAGCCT 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 AGGTTACAGTGGCGGGATCTGGGACAGATTTCACTCTACCCATTAACGCTGTCAACTCT 300

QY 307 GAAGATTTTGGACTTATTACTGTCTACAGGTTTATAGTACCCTCGGACGTTTCGGCCAA 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GAAGATTTTGGCACTTATTATTGTCTAACAGGCTTACAGTACCCCTGAGACTTTGGGCCCA 360

QY 367 GGGACCAAGGTGGAATCAAA 387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GGGACCAAGGTGGAATCAAA 381

RESULT 9
US-08-634-223-16
; Sequence 16, Application US/08634223
; Patent No. 5840298
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.

```


Db 121 ATCACTGCGGGGAGGTGACAGAGATTGCTAGTTAATTGATACAGCAACAACA 180
QY 187 GGAAGAGCTCTTAAGCTCTGATCTATGTGATCCAGTTGGCAAGTGGGGTCCCATCA 246
Db 181 GGGAAAGCCCCCTAAGCTCTGATATATGCTGATCCCAATTTGACACCGTGGGGTCCCGCTCA 240
QY 247 AGGTCAGCGGAGTGATCTGGGACAGAGTTCACTCACCCTGACAGCCCTGACAGCT 306
Db 241 AGGTCAGTGGGGTGGATCTGGGACAGATTTCATCTCCATCAACAGTCTGCAACCT 300
QY 307 GAAGATTTTCCACTTATCTGCTACAGGTTTATAGTACCCCTGGAGCTGGGCCCA 366
Db 301 GAAGATTTTGCACCTATCTATGTCTCAACAGGCTTACAGTACCCCTGGAGCTTTCGGCCCA 360
QY 367 GGGACCAAGGTGGAATCAAA 387
Db 361 GGGACCAAGGTGGAATCAAA 381

RESULT 11

US-08-634-400-16

Sequence 16, Application US/08634400

Patent No. 5939068

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter

APPLICANT: CHAMAT, Soulaïma Salim

APPLICANT: PAN, Li-Zhen

APPLICANT: WALSH, Edward E.

APPLICANT: HEARD, Cheryl Janne

APPLICANT: NEWMAN, Roland Anthony

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND

NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P. O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22131-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/634,400

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/488,376

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-150

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ. ID NO.: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 705 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..705

US-08-634-400-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;
Best Local Similarity 87.4%; Pred. No. 1.3e-86;
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCGCTAAGCTCTGAGGCTCTCTCTGCTGCTCCAGATGCAATGCT 66
Db 1 ATGAGACCCCTGCTAGCTCTGAGGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126
Db 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 127 ATCACTTGACAGGCAAGTACAGACATTAGTATTATTAATTGATACAGCAACAACA 186
Db 121 ATCACTTGACAGGCAAGTACAGACATTAGTATTATTAATTGATACAGCAACAACA 180
QY 187 GGAAGAGCTCTTAAGCTCTGATCTATGTGATCCAGTTTGAAGTGGGGTCCCATCA 246
Db 181 GGGAAAGCCCCCTAAGCTCTGATATATGCTGATCCCAATTTGACACCGTGGGGTCCCGCTCA 240
QY 247 AGGTCAGCGGAGTGATCTGGGACAGAGTTCACTCACCCTGACAGCCCTGACAGCT 306
Db 241 AGGTCAGTGGGGTGGATCTGGGACAGATTTCATCTCCATCAACAGTCTGCAACCT 300
QY 307 GAAGATTTTGCACCTATCTATGTCTCAACAGGCTTACAGTACCCCTGGAGCTTTCGGCCCA 366
Db 301 GAAGATTTTGCACCTATCTATGTCTCAACAGGCTTACAGTACCCCTGGAGCTTTCGGCCCA 360
QY 367 GGGACCAAGGTGGAATCAAA 387
Db 361 GGGACCAAGGTGGAATCAAA 381

RESULT 12

US-08-635-878-16

Sequence 16, Application US/08635878

Patent No. 5955364

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter

APPLICANT: CHAMAT, Soulaïma Salim

APPLICANT: PAN, Li-Zhen

APPLICANT: WALSH, Edward E.

APPLICANT: HEARD, Cheryl Janne

APPLICANT: NEWMAN, Roland Anthony

TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P. O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22131-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/635,878

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/488,376

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-150

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

```

? TELEFAX: (703) 836-2021
? INFORMATION FOR SPO. ID NO.: 16
? SEQUENCE CHARACTERISTICS:
? LENGTH: 705 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..705
?
US-08-635-878-16

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Query Match	78.68;	Score 304.2;	DB 2;	Length 705;
Best Local Similarity	87.48;	Pred. No. 1.3e-86;		
Matches 333; Conservative	0;	Mismatches 48;	Indels 0;	Gaps 0;

Qy	7	ATGAGGGTCCCCGCTCAGACTCTGGGGGCTCTTCGCTCGGGCCAGAGTGCAGATGT	66
Db	1	ATGGAGACCCCTGCTCAGACTCCTGGGGCTCCTGCTACTCTGGCTCCAGAGTGCAGATGT	60
Qy	67	GACATCCAGATGACCCAGCTCCATCTCTCCCTGCTCATCTGTATGGGGAGACAGTCAAC	126
Db	61	GACATCCAGATGACCCAGCTCCATCTCTCCCTGCTCATCTGTGCGAGACAGAGTCAAC	120
Qy	127	ATCAGTTCGACAGGGCAAGTCAGGACATTAGTATTATTTAAATTGGTATCAGCAGAAACA	186
Db	121	ATCAGTTCGCGGGCAGGTCAGAGAGATTGCTAGTATTAAATTGGTATCAGCAGAAACA	180
Qy	187	GGAAGAGCTCTAAGCTCCATGTTATGGTTCATCCAGTTGGCAAAATGGGGGTCCTATCA	246
Db	181	GGGAAAGCCCTTAAGCTCCTATATATGCTGTGATCCAAATTTGCAACCTGGGGTCCGCTCA	240
Qy	247	AGGTTCAAGCGGCAAGTGTGATCTGGAGACAGAGTTCACTCTCAACCGACAGACCTTGACCT	306
Db	241	AGGTTCAATGGCGGGTGGATCTGGAGACAGATTTCACTCTCAACCATCAACAGCTGTCAACT	300
Qy	307	GAGATTTTGGCACTTATTACTGTCCTACAGSTTTAATAGTACCCCTCGAGAGTTGGCCAA	366
Db	301	GAGATTTTGGCACTTATTATTGCAACAGGCTACACAGTACCCCTCGAGCTTTGGCCCA	360
Qy	367	GGGACCAAGGTGGAATCAAA 367	
Db	361	GGGACCAAGGTGGAATCAAA 361	

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1 SOFTWARE: PatentIn Release #1.0, Version #1.30
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3 CURRENT APPLICATION DATA:
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5 APPLICATION NUMBER: US/08/770,057
6
7 FILING DATE:
8
9 CLASSIFICATION:
10
11 PRIOR APPLICATION DATA:
12
13 APPLICATION NUMBER: US 08/488,376
14
15 FILING DATE: 07-JUN-1995
16
17 ATTORNEY/AGENT INFORMATION:
18
19 NAME: Teskin, Robin L.
20
21 REGISTRATION NUMBER: 35,030
22
23 REFERENCE/DOCKET NUMBER: 012712-150
24
25 TELECOMMUNICATION INFORMATION:
26
27 TELEPHONE: (703) 836-6620
28
29 TELEFAX: (703) 836-2021
30
31 INFORMATION FOR SEQ ID NO: 16:
32
33 SEQUENCE CHARACTERISTICS:
34
35 LENGTH: 705 base pairs
36
37 TYPE: nucleic acid
38
39 STRANDEDNESS: single
40
41 TOPOLOGY: linear
42
43 MOLECULE TYPE: DNA (genomic)
44
45 FEATURE:
46
47 NAME/KEY: CDS
48
49 LOCATION: 1..705
50
51 US-08-770-057-16

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Best Local Similarity	-87.4%;	Pred. No. 1.3e-86;		
Matches 333;	Conservative 0;	Mismatches 48;	Indels 0;	Gaps 0;

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Db	1	ATGAGAGACCCCTGCTCAGCTCTGGGGGCTCTGCTACTCTGGCTCCGAGGTGCCAATG	60
Oy	67	GACATCCAGATGACCCAGCTCCATCTTCCCTGTCGATCTGTAGGGGGACAGATCAC	126
Db	61	GACATCCAGATGACCCAGCTCCATCTTCCCTGTCGATCTGTGCGAGACAGATCAC	120
Oy	127	ATCATTCCAGGGCAGTCAGACATTAGTATTATTAAATTGGTATCAGCAGAAACA	186
Db	121	ATCATTCTCCGGGAGGTCAGAGGATTGCTAGTATTAAATTGGTATCAGCAGAAACA	180
Oy	187	GAAAGAGCTCTAAAGCTCCATGATGATGTCACAGTTTGCAGAACTGGGGTCCCATCA	246
Db	181	GGGAAAGCCCTTAAGCTCTCTATATATGCTGGATTCCAATTTGGCAGCTGGGGTCCGTCA	240
Oy	247	AGGTTACAGCGGCAGTGATCTGGGACAGAGTTCACTCTCAACCGTCAGACAGCTGCACCT	306
Db	241	AGGTTCACTGGCGGGTGATCTGGGACAGATTTCACTCTCAACATCAACAGTGTGCACCT	300
Oy	307	GACGATTTTGGACTTATTACTGTCCTACAGTTTATAGTACCCCTCGGACGTTGGCCAA	366
Db	301	GAGGATTTTGGCACTTAATTTGTCACAGCTTACAGTACCCCTCGACTTTTGGCCCA	360
Oy	367	GGGACCAAGTGGAAATCAA 387	
Db	361	GGGACCAAGTGGAAATCAA 381	

RESULT 14
US-09-335-697B-16
; Sequence 16, Application US/09335697B
; Patent No. 6200804
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; CHAMAT, Soulatima Salim
; PAN, Li-Zhen
; WALSH, Edward E.
; HEARD, Cheryl Janne
; NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-0090400S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 420:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-420

Query Match 78.0%; Score 302; DB 4; Length 420;
Best Local Similarity 86.9%; Pred. No. 5.2e-86;

Matches 332; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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QY 66 TGACATCCAGATGACCATTCCTCCCTGCTGCTGCTGCCAGTGCCAGATG 125
DB 72 CGACATCCAGATGACCATTCCTCCCTGCTGCTGCTGCCAGTGCCAGATG 131
QY 126 CATCACTTCAGGCAAGTCAGCATTTAGTATTTAAATTGGTATCAGCAGAAAC 185
DB 132 CATCACTTCGCGGCGAGTAGAGATTTAGCAGCTGTTAGCCTGGTATCAGCATAAAC 191
QY 186 AGGAAAGCTCCTAACCTCTGATCTATGTGATCCAGTTTGCAGAGTGGGTCCATC 245
DB 192 AGGTAAGACACCTACCTCTGATCTATGTGATCCAGTTTGCAGAGTGGGTCCATC 251
QY 246 AAGGTCAGGGGAGTGATCTGGGACAGAGTTCACCTCAGCCGTCAGCAGCC 305
DB 252 AAGGTCAGGGGAGTGATCTGGGACAGAGTTCACCTCAGCCGTCAGCAGCC 311
QY 306 TGAAGATTTGCGACTTATTAAGTCTACAGGTTTATAGTACCCCTCGAGGTTGCGCA 365
DB 312 TGAAGATTTGCAATTAAGTCTACAGGTTTATAGTACCCCTCGAGGTTGCGCA 371
QY 366 AGGAGCAAGGTGAATCAAA 387
DB 372 GGGAACCAAGCTGGAGATCAAA 393

Search completed: September 23, 2002, 18:00:53
Job time: 3224 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:50:12 : Search time 2581.68 Seconds
(without alignments)
3331.477 Million cell updates/sec

Title: US-09-019-441-4

Perfect score: 411
Sequence: 1 ATGGAGTTGGCGTCTGAGCTG.....TCTGTGTCACCGTCTCTCA 411

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

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2: gb_hlg:*
3: gb_in:*
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32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	283.6	69.0	437	9	HUMIGHVAK	M18513 Human (feta
3	279.4	68.0	415	9	HSBEL20	X81725 H.sapiens r
4	278.6	67.8	411	9	HSBEL28	X81726 H.sapiens r
5	277.4	67.5	417	9	HSBEL34	X81729 H.sapiens r
6	276.6	67.2	423	9	AF062285	AF062285 Homo sapi
7	275.8	67.1	402	9	AF062280	AF062280 Homo sapi
8	275.2	67.0	408	9	HSVHIC10	AJ234277 Homo sapi
9	275.2	67.0	470	9	HUMIGHCXE	M34024 Human fetal
10	274.6	66.7	411	9	HSB234278	AJ234278 Homo sapi
11	273.8	66.6	411	9	HSE5433	Z14201 H.sapiens r
12	273.8	66.6	437	9	HSIGHX13	X65895 H.sapiens m
13	272.8	66.4	420	9	HSBEL56	X81734 H.sapiens r
14	272.4	66.3	417	9	HSB234298	AJ234298 Homo sapi
15	272.4	66.3	414	9	AF062269	AF062269 Homo sapi
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17	271.2	66.0	423	9	AF062212	AF062212 Homo sapi
18	270.4	65.8	463	9	AF173920	AF173920 Macaca mu
19	270.4	65.7	441	9	HSR0221	X81751 H.sapiens r
20	269.8	65.6	426	9	AF062206	AF062206 Homo sapi
21	269.8	65.6	463	9	AF173919	X65900 H.sapiens m
22	269.6	65.6	420	9	HSIGHX18	AF062205 Homo sapi
23	269.6	65.6	423	9	AF062205	AF062205 Homo sapi
24	269.6	65.6	423	9	AF174012	AF174012 Homo sapi
25	269.2	65.5	448	9	HSE5434	Z14202 H.sapiens r
26	268.4	65.3	487	9	HSIG487	X61013 Human Immun
27	268.4	65.3	488	9	HSIG488	X61014 Human Immun
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31	267.4	65.1	411	6	BD004423	BD004423 Ameliorat
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33	267.4	65.1	411	6	BD004540	BD004540 Therapeut
34	267.4	65.1	411	6	BD008373	BD008373 Inhibiti
35	267.4	65.1	411	6	E23343	E23343 Antibody ag
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37	266.8	64.9	429	9	AF062182	AF062182 Homo sapi
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41	266.4	64.8	461	9	HSE54310	Z14200 H.sapiens r
42	266.4	64.7	450	9	HSU24080	U24080 Human Immun
43	265.8	64.7	437	9	HSE5435	Z14203 H.sapiens r
44	265.8	64.7	455	9	HUMIGH2M	L33852 Human Immun
45	265.6	64.6	486	9	HSIG486	X61011 Human Immun

ALIGNMENTS

RESULT 1
LOCUS HUMIGHADC 405 bp mRNA linear PRI 09-NOV-1994
DEFINITION Human Ig rearranged gamma-chain mRNA V-region, 5' end of cds (from clone STIP15).

ACCESSION L06912
VERSION L06912.1 GI:185008
KEYWORDS V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain; processed gene.
SOURCE Homo sapiens (tissue library: BC) Female Adult Synovium CDNA to mRNA.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Bridges, S.L., Jr., Lee, S.K., Koopman, W.J. and Schroeder, H.W., Jr.
TITLE Analysis of immunoglobulin gamma heavy chain expression in synovial tissue of a patient with rheumatoid arthritis

JOURNAL Arthritis Rheum. 36 (5), 631-641 (1993)
MEDLINE 93256941
FEATURES Location/Qualifiers

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/db_xref="GDB:G00-128-528"
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Best Local Similarity 83.5%; Pred. No. 8.9e-68;
Matches 343; Conservative 0; Mismatches 62; Indels 6; Gaps 1;

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QY 121 TGGCAGCCTCGGGTTCAAGTTCACTTCAATTAATCACTAGATGAGTGGTCCG 180
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DB 295 TATCTCAATTAAGAACCTGAGAGCGAGAGACAGGCGCATATTACTGTGGAGAGG 354

QY 361 ACACAGGGGTCTACCTCTGGGGCGAGGAGTCTGTGTCACCTCTCTCA 411
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DB 355 GTTGAAGAGGGCTACTGTGGGCGAGGAGAACCTGTGTCACCTCTCTCA 405

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HUMIGHVAK      437 bp      mRNA      linear      PRI 09-NOV-1994
DEFINITION      Human (fetal) rearranged Igm chain VDJ-region mRNA, clone 30P1.
ACCESSION      M18513
VERSION      M18513.1 GI:185539
KEYWORDS      C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
      immunoglobulin mu-chain; processed gene; variable region subgroup
      VH-III.
SOURCE      Homo sapiens foetus liver cDNA to mRNA.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 437)

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AUTHORS      Schroeder, H.W. Jr., Hillson, J.L. and Perlmuter, R.M.
TITLE      Early restriction of the human antibody repertoire
JOURNAL      Science 238 (4828), 791-793 (1987)
MEDLINE      88042812
COMMENT      Draft entry and computer-readable sequence [1] kindly submitted by
      Schroeder 08-NOV-1988.
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ORIGIN      Chromosome 14q32.

Query Match      69.0%; Score 283.6; DB 9; Length 437;
Best Local Similarity 83.6%; Pred. No. 4.2e-66;
Matches 351; Conservative 0; Mismatches 54; Indels 15; Gaps 2;

QY 1 ATGAGATTGGGCTGAGCTGGTTTCTCTCTTTTGAAGGTGTCAGTGCAG 60
    |||||||
DB 24 ATGAGATTGGGCTGAGCTGGTTTCTCTCTTTTGAAGGTGTCAGTGCAG 83

QY 61 GTGCAGCTGGTGAAGTCTGGGGGCGCTGGCAAGCCTGGGCTCCAGACTCTG 120
    |||||||
DB 84 GTGCAGCTGGTGAAGTCTGGGGGCGCTGGCAAGCCTGGGCTCCAGACTCTCC 143

QY 121 TGGCAGCCTCGGGTTCAAGTTCACTTCAATTAATCACTAGATGAGTGGTCCG 180
    |||||||
DB 144 TGTGACAGCCTCTG-----GATTCACCTTTAGCAGCTATGCTGAGTGGTCCG 197

QY 181 GCTCCAGGGGAGGGGCTGAGTGGTCTCACTATTAGTAGTGGTGCATCCACATGG 240
    |||||||
DB 198 GCTCCAGGGGAGGGGCTGAGTGGTCTCACTATTAGTAGTGGTGCATCCACATGG 257

QY 241 TACGACAGCTCCGTGAAGGCGAATTCACCATCTCCAGAGAGAGCCACACACTG 300
    |||||||
DB 258 TACGACAGCTCCGTGAAGGCGCGTTCACTCATCAGAGACAAATTCAGAGACAGCTG 317

QY 301 TTCTTCAATTAAGAACCTGAGAGCTGAGAGACAGGCTGTATTACTGTGGGA----- 355
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DB 318 TATCTCAATTAAGAACCTGAGAGCGAGAGACAGGCGCATATTACTGTGGGAAGAT 377

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LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
356	-----GCTGACTACAGGCTGACATCCCTGGGGCCGAGAGCTGTCACCTGCTCA	411									
378	GCCGCGTGGGCTTCGGGCTTTGACTACTGGGGCCAGGAGACCTGTCACCTCTCTCA	437									
RESULT 3	HSBEL20	415 bp	mRNA	Linear	PRI 29-FEB-1996						
LOCUS	H.sapiens rearranged VDJ region (BEL20).										
DEFINITION	X81725										
VERSION	X81725.1	GI:1212930									
KEYWORDS	diversity region; immunoglobulin heavy chain; joining region; variable region; VH-3 family.										
SOURCE	human.										
ORGANISM	Homo sapiens										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
TITLE	1 (bases 1 to 415)										
JOURNAL	Millil,M., Schiff,C., Fougereau,M. and Tonnelle,C.										
COMMENT	The VDJ repertoire expressed in human preB cells reflects the selection of bona fide heavy chains										
FEATURES	Eur. J. Immunol. 26 (1), 63-69 (1996)										
LOCUS	96152725										
DEFINITION	2 (bases 1 to 415)										
AUTHORS	Tonnelle,C.										
TITLE	Direct Submission										
JOURNAL	Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie										
COMMENT	Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE										
FEATURES	Related sequences: X65741, X65883 to X65920.										
SOURCE	Location/Qualifiers										
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DEFINITION	/organism="Homo sapiens"										
AUTHORS	/db_xref="taxon:9606"										
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DEFINITION	/clone="BEL 20"										
AUTHORS	1. .57										
TITLE	/product="immunoglobulin heavy chain V region"										
JOURNAL	346. .372										
COMMENT	/product="immunoglobulin heavy chain D segment"										
FEATURES	373. .415										
LOCUS	/product="immunoglobulin heavy chain J segment"										
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AUTHORS	ORIGIN										
TITLE	sig.peptide										
JOURNAL	V_region										
COMMENT	D.segment										
FEATURES	J_segment										
LOCUS	Query Match										
DEFINITION	Best Local Similarity 82.9%; Score 279.4; DB 9; Length 415;										
AUTHORS	Matches 349; Conservative 0; Mismatches 56; Indels 16; Gaps										
TITLE	1 ATGAGATTGGCTGAGCTGGGCTTTCCTGTTCTGTTCCCTTTGAAAGGTGTCAGTGTGAG					</					

DB	235	TACGAGACCTCCGGGAAGGGCGGANTTACCAATTCCTCAGACAAACGCCAAGAACTACTG	294
QY	301	TTTCTTCAATGAACACAGCTTAGAGACTAGACACAGCGTGTCTATTACTGTGCGAGCTTG	360
Db	295	TATCTGAAATGAACAGCCTTAGAGCCAGGACACAGCGTGTATTACTGTCAAACTAG	354
QY	361	ACTA-----CAGGCTCTGACTCTCTGGGGCCAGGAGAGCTGTCACCGTCTCTC	410
Db	335	AGGAGTCTCCGAGAGCTCTTCTTTGACTACTGAGGGCCAGGAACTCTGTACCTCTCTC	414
QY	411	A	411
Db	415	A	415
RESULT	4		
LOCUS	HSBEL28	411 bp	linear PRI 29-FEB-1996
DEFINITION	H.sapiens rearranged VDJ region (BEL28).		
ACCESSION	X81726		
VERSION	X81726.1	GI:1212931	
KEYWORDS	diversity region; immunoglobulin heavy chain; joining region; variable region; VH-3 family.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 411)		
TITLE	Millil,M., Schiff,C., Fougereau,M. and Tonnelle,C.		
JOURNAL	The VDJ repertoire expressed in human preB cells reflects the selection of bona fide heavy chains		
MEDLINE	Eur. J. Immunol. 26 (1), 63-69 (1996)		
REFERENCE	96152725		
AUTHORS	2 (bases 1 to 411)		
TITLE	Tonnelle,C.		
JOURNAL	Direct Submission		
COMMENT	Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie		
FEATURES	Marseille-Limny, Case 906, 13288 Marseille, Cedex 9, FRANCE		
source	Related sequences: X65741, X65883 to X65920.		
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	/cell_type="pre B-lymphocytes"		
	/clone_id="BEL"		
	/clone="BEL 28"		
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	58. .352		
	/product="immunoglobulin heavy chain V region"		
	353. .362		
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	363. .411		
	/product="immunoglobulin heavy chain J segment"		
	BASE COUNT 83 a 103 c 127 g 98 t		
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Query Match	67.8%	Score 278.6;	DB 9; Length 411;
Best Local Similarity	83.0%;	Pred. No. 9.5e-65;	
Matches 346; Conservative	0; Mismatches 59;	Indels 12; Gaps	2;
QY	1	ATGGAGTTTGGGCTGAGCGGGTTTCCCTTCTTCTTCTTCAAGGTCCTCAGTGTAG	60
Db	1	ATGGAGTTTGGGCTGAGCTGAGCTTTTCTTCTTCTTCAAGGTCCTCAGTGTAG	60
QY	61	GTGCACTGTGTGAGCTGTGGGGCGGCTTGGCAAAAGCTGGGGGTCCTGAGACTTGG	120
Db	61	GTGCACTGTGTGAGCTGTGGGGCGGCTTGGCAAAAGCTGGGGGTCCTGAGACTTGG	120
QY	121	TGCGCAGCCTCCGGGTTAGGTTCACTTCAATACTACTACATGAGACTGGTCCGCCAG	180

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Db 121 TGTGCACCTCTG-----GATTCACCTTAGCAGCTATGCGCATGAGCTGGTCCGCAG 174
Oy 181 GCTCCAGGGAGGGGCTGGAGTGGGTCTCAAGTATTAGTAGTATGATGGTATCCACATGG 240
Db 175 GCTCCAGGAGGAGGGGCTGGAGTGGGTCTCAAGTATTAGTAGTATGATGGTATCCACATGG 234
Oy 241 TACGACACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 TACGACACTCCGTGAAGGCGGCTTACCATCTCCAGAGAGATTCACATTAACACACTG 294
Oy 301 TTTCTTAAATGAACACCTGAGAGCTGAGACACGCGCTGTATTACTGTGCG----- 354
Db 295 TACTTGAATGAACACCTGAGAGCGGAGACGCGCGGTATTACTGTGCGAAACCC 354
Oy 355 AGCTGACTACGAGGCTGACTCCTGGGGCAGGAGTCCGTGGTCCAGCTCTCTCA 411
Db 355 AACTGTTCAACTGTTCGACCCCTGGGGCCAGGGAACCCGTGTCTCTCTCA 411

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RESULT 5
HSEBL34 417 bp mRNA linear PRI 29-FEB-1996
LOCUS HSEBL34
DEFINITION H.sapiens rearranged VDJ region (BEL34).
ACCESSION X81729
VERSION X81729.1 GI:1212933
KEYWORDS diversity region; immunoglobulin heavy chain; joining region;
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 417)
AUTHORS M1111.M., Schiff,C., Fougereau,M. and Tonnellet,C.
TITLE The VDJ repertoire expressed in human preB cells reflects the
JOURNAL Eur. J. Immunol. 26 (1), 63-69 (1996)
MEDLINE 96152725
REFERENCE 2 (bases 1 to 417)
AUTHORS Tonnellet,C.
TITLE Direct Submision
JOURNAL Submitted (15-SEP-1994) C. Tonnellet, Centre d'Immunologie
Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE
COMMENT Related sequences: X65741, X65883 to X65920.
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1. 417
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1..57
sig_peptide
58..352
V_region
353..374
D_segment
375..417
J_segment
/product="immunoglobulin heavy chain V region"
/product="immunoglobulin heavy chain D segment"
/product="immunoglobulin heavy chain J segment"
BASE COUNT 92 a 94 c 127 g 104 t
ORIGIN

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Query Match 67.5%; Score 277.4; DB 9; Length 417;
Best Local Similarity 82.5%; Pred. No. 2e-64;
Matches 349; Conservative 0; Mismatches 56; Indels 18; Gaps 2;

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Oy 1 ATGAGATTGGGCTGAGCTGGTTTCTGTTCTCTTTGAAGGCTGTCAGTGTGAG 60
Db 1 ATGAGATTGGGCTGAGCTGGTTTCTGTTCTCTTTGAAGGCTGTCAGTGTGAG 60

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Oy 61 GTGCAGCTGTGAGTCTGGGGGCGGCTTGGCAAGCTGGGGGCTCCAGACTCTGG 120
Db 61 GTGCAGCTGTGAGTCTGGGGGCGGCTTGGCAAGCTGGGGGCTCCAGACTCTCC 120
Oy 121 TGCCGACCTCCGGGTTTCAGTTACCTTCATTAATCACTATGACTGGTCCGCAG 180
Db 121 TGTGCACCTCTG-----GATTCACCTTCAGTATTAGTAAAGAACTGGTCCGCAG 174
Oy 181 GCTCCAGGGAGGGGCTGGAGTGGGTCTCAAGTATTAGTAGTATGATGGTATCCACATGG 240
Db 175 GCTCCAGGAGGAGGGGCTGGAGTGGGTCTCAAGTATTAGTAGTATGATGGTATCCACATGG 234
Oy 241 TACGACACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 TACGACACTCTTAAGAGGGCGCATTCACCATCTCCAGAGAGAACGCCAACACTG 294
Oy 301 TTTCTTAAATGAACACCTGAGAGCTGAGACACGCGCTGTATTACTGTGCG----- 354
Db 295 TATCTGAAATGAACACCTGAGAGCGGAGACGCGCGGTATTACTGTGCGAAACCT 354
Oy 355 -----AGCTTACTACAGGCTGACTCCTGGGGCAGGAGTCCGTGACCGTCTCC 408
Db 355 AGAGGAAGTGGGAGCTCTTGTACTACTGGGGCCAGGGAACCTGTCTACCGTCTCC 414
Oy 409 TCA 411
Db 415 TCA 417

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RESULT 6
AF062285 423 bp mRNA linear PRI 09-MAY-2001
LOCUS AF062285
DEFINITION Homo sapiens clone Xu-57 immunoglobulin heavy chain variable region
(IGH) mRNA, partial cds.
ACCESSION AF062285
VERSION AF062285.1 GI:3171042
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS Wang,X. and Stollari,B.D.
TITLE Immunoglobulin VH gene expression in human aging
JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE 99459182
PUBMED 10527689
REFERENCE 2* (bases 1 to 423)
AUTHORS Wang,X. and Stollari,B.D.
TITLE Direct Submision
JOURNAL Submitted (30-APR-1998) Biochemistry Department, Tufts University
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES
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1. 423
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="blood"
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gene
CDS

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JOURNAL Br. J. Haematol. 107 (3), 625-640 (1999)
MEDLINE 20050318
REFERENCE 2 (bases 1 to 411)
AUTHORS Noppe,S.M.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-1998) Noppe S.M., Laboratory of Physiology, Free University of Brussels Laarbeeklaan 103/E, 1090 Brussels, BELGIUM

FEATURES
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BASE COUNT 90 a 100 c 124 g 97 t
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Query Match 67.0%; Score 275.4; DB 9; Length 411;
Best Local Similarity 82.5%; Pred. No. 6.9e-64;
Matches 344; Conservative 0; Mismatches 61; Indels 12; Gaps 2;

QY 1 ATGAGTTTGGGCTGAGCTGGTTTCCTTCTGCTCTTTTGAAGAGTCCAGGTCAG 60
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Db 1 ATGAGTTTGGGCTGAGCTGGTTTCCTTCTGCTCTTTTGAAGAGTCCAGTGTAG 60
QY 61 GTGACGCTGTGAGTCTGGGGGCGCTGGCAAGCCCTGGGGGCTCCCTGAGACTCTG 120
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Db 61 GTGACGCTGTGAGTCTGGGGGCGCTGGCAAGCCCTGGGGGCTCCCTGAGACTCTC 120
QY 121 TGCGCAGCTCCGGGTTTCAGGTTCACTTCAATACATCACTGATGAGTGGTCCGCCAG 180
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Db 121 TGTCACGCTCTG-----GGCTACCGCTCAGTACGACATCAATGAGCTGGTCCGCCAG 174
QY 181 GCTCCAGGGGAGGGGCTGAGTGGTCTCAAGTATAGTAGTATGATGATC-----C 234
|||||
Db 175 GCTCCAGGGGAGGGGCTGAGTGGTCTCAAGTATAGTAGTATGATGATGATC-----C 234
QY 235 ACATGAGTACGACACTCCGTTGAAGGCGATTCACATCTCCAGAGAACGCCAACAC 294
|||||
Db 235 GCATACACGACACTCCGTTGAAGGCGATTCACATCTCCAGAGAACGCCAACAC 294
QY 295 ACACTGTTTCTTCAATGACAGCCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGCG 354
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Db 295 ACACTGTTTCTTCAATGACAGCCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGCG 354
QY 355 AGCTTACTACAGGCTGACTCCTGGGGCGAGGAGTCTGTACACGCTCTCTCA 411
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Db 355 AGATTGAGAGAGTGGCTTGAAGCTGTGGGGCCAAAGGACACAGGCTCCTCTCA 411

RESULT 9
HSVHIC10
LOCUS H.sapiens mRNA for immunoglobulin heavy chain V-region (clone
DEFINITION CDN31C10).
ACCESSION 247226
VERSION 247226.1 GI:1197316
KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 113)
AUTHORS Demaison,C., David,D., Letourneur,F., Zouali,M., Saragosti,S. and
These,J.

TITLE A cDNA/anchor-PCR approach to analyse the human VH gene repertoire
JOURNAL expressed by peripheral CD19+ B cells reveals a strong bias usage
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 408)
TITLE Direct Submission
JOURNAL Submitted (16-DEC-1994) Christophe Demaison, Immunologie, Unite
d'Immunogenetique Cellulaire-Institut Pasteur, 25, rue du Docteur
Roux, Paris, 75015, FRANCE
REFERENCE 3 (bases 1 to 408)
AUTHORS Demaison,C., David,D., Letourneur,F., These,J., Saragosti,S. and
Zouali,M.

TITLE Analysis of human VH gene repertoire expression in peripheral CD19+
JOURNAL B cells
MEDLINE Immunogenetics 42 (5), 342-352 (1995)
FEATURES 96006568
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V-region /product="immunoglobulin variable region"
BASE COUNT 83 a 101 c 129 g 95 t
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Query Match 67.0%; Score 275.2; DB 9; Length 408;
Best Local Similarity 82.6%; Pred. No. 7.9e-64;
Matches 342; Conservative 0; Mismatches 63; Indels 9; Gaps 2;

QY 1 ATGAGTTTGGGCTGAGCTGGTTTCCTTCTGCTCTTTTGAAGAGTCCAGTGTAG 60
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Db 1 ATGAGTTTGGGCTGAGCTGGTTTCCTTCTGCTCTTTTGAAGAGTCCAGTGTAG 60
QY 61 GTGACGCTGTGAGTCTGGGGGCGCTGGCAAGCCCTGGGGGCTCCCTGAGACTCTG 120
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Db 61 GTGACGCTGTGAGTCTGGGGGCGCTGGCAAGCCCTGGGGGCTCCCTGAGACTCTC 120
QY 121 TGCGCAGCTCCGGGTTTCAGGTTCACTTCAATACATCACTGATGAGTGGTCCGCCAG 180
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Db 121 TGTCACGCTCTG-----GATTTCACCTTGAAGCAGTATGACAGTGGTCCGCCAG 174
QY 181 GCTCCAGGGGAGGGGCTGAGTGGTCTCAAGTATAGTAGTATGATGATGATC-----C 240
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Db 175 GCTCCAGGGGAGGGGCTGAGTGGTCTCAAGTATAGTAGTATGATGATGATGATC-----C 234
QY 241 TACGACACTCCGTTGAAGGCGAATTCACATCTCCAGAGAACGCCAACACACTG 300
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Db 241 TACGACACTCCGTTGAAGGCGAATTCACATCTCCAGAGAACGCCAACACACTG 300
QY 235 TACGACACTCCGTTGAAGGCGGCTTCAACATCTCCAGAGAACGCCAACACACTG 294
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Db 235 TACGACACTCCGTTGAAGGCGGCTTCAACATCTCCAGAGAACGCCAACACACTG 294
QY 301 TTTTCTTAATGACACACTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGAGCTTG 360
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Db 295 TATCTGCAAAATGACACACTGAGAGCCGAGACAGGCTGTCTATTACTGTGCAAAAGAT 354
QY 361 ACTACAGGCTC---TGACTCCTGGGGCAGGAGTCTGTGACACGCTCTCTCA 411
|||||
Db 355 GGCCCTTGAACCGAGACTGTGGGCCAGGAAACCTGTGTACCGCTCTCTCA 408

RESULT 10
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LOCUS HUMIGHCXE
DEFINITION Human fetal Ig heavy chain variable region (clone M43) mRNA,
partial cds.
ACCESSION M34024
VERSION M34024.1 GI:185267
KEYWORDS D-region; J-region; V-region; immunoglobulin heavy chain; processed
gene.

Db	351	TATCTGCAAAATGACACGCTTGAGAGCCGAGACACGCGCCGTATATTTACTGTGCGCAAAAAG	410
Oy	356	---GCTTGACTACAGGGTCTGACTCTCTGAGGCGCAGGAGATCCTGTACCGTCTCTCA	411
Db	411	GACTGGAAACGACACATGTTGCACTCCCTCGGGGCCAGGGAACCTGTGTCACCGTCTCTCA	470
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DEFINITION	Homo sapiens mRNA for Ig heavy chain variable region, clone C9.		
ACCESSION	AJ234278		
VERSION	AJ234278.1	GI:3821218	
KEYWORDS	heavy chain; immunoglobulin superfamily; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Noppe,S.M., Heltman,C., Bakkus,M.H., Brissinck,J., Schots,R. and Thielemans,R.		
TITLE	The genetic variability of the VH genes in follicular lymphoma: the impact of the hypermutation mechanism		
JOURNAL	Br. J. Haematol. 107 (3), 625-640 (1999)		
MEDLINE	20050318		
REFERENCE	2 (bases 1 to 411)		
AUTHORS	Noppe,S.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-Oct-1998) Noppe S.M., Laboratory of Physiology, Free University of Brussels laarbeeklaan 103/E, 1090 Brussels, BELGIUM		
FEATURES	Location/Qualifiers		
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V-region	<1..>411		
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BASE COUNT	90 a 101 c 123 g 97 t		
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Query Match	66.6%; Score 273.8; DB 9; Length 411;		
Best Local Similarity	82.3%; Pred. No. 1.9e-63;		
Matches 343; Conservative 0; Mismatches 62; Indels 12; Gaps 2;			
Oy	1	ATGAGTTGGGCTGAGTGGGTTTCTGTCTCTCTTTGAAAGGTGTCAGTGTGAG	60
Db	1	ATGGAGTTTGGGCTGAGCTGGCTTTCCTGTGTGCTATTTAAAGGTGTCAGTGTGAG	60
Oy	61	GTGCGAGTGTGGAATCTGGGGGGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTGTGG	120
Db	61	GTGCGAGTGTGGAATCTGGAGAGGAGCTTGATCCAGCCTGGGGGGTCCCTGAGACTTCC	120
Oy	121	TGCGCAGCCTCGGGTTTACGTTCACCTTCAATAAATCTACTACATGAGCTGGTCCGCAG	180
Db	121	TGTGAGGCTCTG-----GGCTACCGCTCAGATGACTACACTATGAGCTGGGTCCGCAG	174
Oy	181	GCTCCAGGCGAGGGCTGAGTGGTCTCAGCTATTAGTACTAGTGTGATCC-----C	234
Db	175	GCTCCAGGGAAGGGGCTGAGAGGTGCTCTACATTATTTATGTGTGGTGAACAACATACTAC	234
Oy	235	ACATGTACGACAGATCCTCGTGAAGGCGAGATTCAACATCTCAAGAGAAAGCCAAACAC	294
Db	235	GCATCTACGACAGATCTCGTGAAGGCGCGATTCAACATCTCCAGACAAATTCAAAGAAC	294
Oy	295	ACACGTGTTCTTCAAAATACACGCTTGAGAGCTGAGACACAGGGCTGTCTATTACTGTGCG	354

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Db      295  ACACATATATCTTCAAAAGAACACCCCTGACAGTGAGAGACAGCCCGATATATTTACTGTGCG 354
OY      355  AGATTGACACAGGAGTCTGACTCTGGGGGCCAGAGAGTCTTGGTCCACCGTCTCTCA 411
Db      355  AGATTGAGAGAGTGCCCTTGACGTCTGTGGGCCCAAGGAGACCGGTACCGTCTCTCTCA 411

RESULT 12
LOCUS   HSE5433                      437 bp    mRNA    linear    PRI 15-MAR-1993
DEFINITION H.sapiens rearranged Ig heavy chain variable region (VDJ).
ACCESSION Z14201 X65741
VERSION   Z14201.1 GI:30961
KEYWORDS  Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Ig variable region; immunoglobulin.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 437)
AUTHORS   Tonnelle,C.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUN-1992) C. Tonnelle, Centre d'Immunologie
REFERENCE 2 (bases 1 to 437)
AUTHORS   Cuisinier,A.M., Gauthier,L., Boubill,L., Fougereau,M. and Tonnelle,C.
TITLE     Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in fetal liver
JOURNAL   Eur. J. Immunol. 23 (1), 110-118 (1993)
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                     /translation="MEFGLSMFLVAIIKGNOCVOYLESGGGLVHPGSLRLSCAAS
                     GFTSSYAMSWRQAPRGKLEWYSAISSGGSTYYSDSVKGRLLTISRDNSKNTLYDM
                     NSLRADIDAVIYCAKRRDIDYWGCGTLVVS"
                     93..386
                     /note="variable region"
                     387..398
                     /note="diversity region"
                     399..437
                     /note="joining region"
BASE COUNT  93 a      104 c      136 g      104 t
ORIGIN
Query Match      66.6%; Score 273.8; DB 9; Length 437;
Best Local Similarity 82.7%; Pred. No. 1.9e-63;
Matches 340; Conservative 0; Mismatches 62; Indels 9; Gaps 2;

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OY      121  TGGCAGACCTCCGGGTTTCAGCTTCACTCAATTAAGTACAGTGGTCCGCCAG 180
Db      156  TGTGACAGCTCTG-----GATTCACCTTTAGACGATATGAGCTGGTCCGCCAG 209
OY      181  GCTCCAGGAGGAGGCTGGAGTGGTCTACGATTAAGTATGATGATCCCAATGG 240
Db      210  GCTCCAGGAGGAGGCTGGAGTGGTCTACGATTAAGTATGATGATGATCCCAATGG 269
OY      241  TACGACAGCTCCGTGAAGGAGCAGATTACACATCTCCAGAGAGAACCCCAACACACTG 300
Db      270  TACTCAGACCTCGCTGAAGGCGCGCTCACCATCTCCAGAGACATTCGAAGAACAGCTG 329
OY      301  TTCTCTCAATTAAGACAGCTGAGAGCTGAGACACGCGTCTATTACTGTGCGAGCTTG 360
Db      330  TATCTCAATTAAGACAGCTGAGAGCTGAGACACGCGCTATTATTACTGTGCGAGACTAG 389
OY      361  ACTACAGGCTGTGACCTCGGGGCGAGGGAGTCCGTGTCACCGTCTCCCTCA 411
Db      390  ---CGGATCTAGACTAGTGGGCCAGGGACCTGTGTCACCGTCTCTCA 437

RESULT 13
LOCUS   HSIGHXX13                      420 bp    mRNA    linear    PRI 26-JUL-1997
DEFINITION H.sapiens mRNA for XLA Ig heavy chain VDJ region (IE 3-12).
ACCESSION X65895 S58681
VERSION   X65895.1 GI:395092
KEYWORDS  diversity region; Ig heavy chain; immunoglobulin; joining region; variable region; human.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 420)
AUTHORS   Schiff,C.
TITLE     Direct Submission
JOURNAL   Submitted (08-APR-1992) C. Schiff, Centre d'Immunologie de
REFERENCE 2 (bases 1 to 420)
AUTHORS   M1111,M., Le Delst,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.
TITLE     Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
JOURNAL   J. Clin. Invest. 91 (4), 1616-1629 (1993)
FEATURES
     source             location/Qualifiers
                     1..420
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /tissue_type="bone marrow"
                     /cell_type="pre-B"
                     /clone_lib="LE library"
                     /clone="LE 3-12"
                     1..57
                     /note="variable region"
                     58..352
                     /note="diversity region"
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BASE COUNT  84 a      99 c      135 g      102 t
ORIGIN
Query Match      66.4%; Score 272.8; DB 9; Length 420;
Best Local Similarity 81.7%; Pred. No. 3.5e-63;
Matches 348; Conservative 0; Mismatches 57; Indels 21; Gaps 2;

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gene	1. .414	/gene="WarLVDU"
V_region	<1. .>.414	/gene="WarLVDU"
BASE COUNT	91 a	90 c 130 g
ORIGIN		103 t

Query Match	66.38;	Score 272.4;	DB 9;	Length 414;
Best Local Similarity	81.98;	Pred. No. 4.5e-03;		
Matches 344;	Conservative 0;	Mismatches 61;	Indels 15;	Gaps 2

QY	1	ATGAGATTGGGCGAGCTGGGTTTCCCTTTCTCTCTCTTTGAAAGGTGTCAGCTGAG	60
Db	1	ATGGAATTCCGGGCGTACGCTGGGTTTCTCTTCTCTATTATTTAGAAGGTGCCAGTGTAG	60
QY	61	GTCGACGTGTGGAATCTGGGGGGCGGCTTGGCAAGCCTGGGGGTCCTCGAGACTCTGG	120
Db	61	GTCGAGCTGTGTGAATCTGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCGTAGACTCTCC	120
QY	121	TGCGGACCTTCGGGCTTCAGCTTACCTTCANTACTACTACATGAGCTGGTCCGCAG	180
Db	121	TGTGTAGCCTCTG-----GATTCACCTTTAGTGTATATGACATGAACCTGGTCCGCCAG	174
QY	181	GCTCCAGGCGGGGGCTGGGAATGGGTCGACGTATGTATGTATGTGTGTATCCACATGG	240
Db	175	ACTCCAGGGAAGGGGCTGGATGGGTTTCACTATTGTATGTATGTATGTACTTACCACTAC	234
QY	241	TACGCAAGCTCCGTGAAGGGGAGATTACCATCTCCAGAGAGAAGCGCAACACACTG	300
Db	235	TACGGAAGCTCTGTGAAGGGCGAATCCACCATCTCCAGAGACAATGCCAAGAACTCACTG	294
QY	301	TTTCTTCAATGAACAGCCTTAGAGCTGAGAGACAGGCTGTCTATTACTGTGGAGCTTG	360
Db	295	GATCTGCAAAAGAACAGCCTTAGAGAGAGACACAGGCTGTGTATTACTGTGGAGGCTCG	354
QY	361	ACTACAGAGTC-----TGACTCCCTGGGGCCAGGAGAGCCGCGTACACGTCCTCTCA	411
Db	355	GACATATGGTTTGGGAGATATATGACTACTGGGGGCGAGGAACCCCTGGTACACGTCCTCTCA	414

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Search completed: September 23, 2002, 17:50:15
Job time: 6869 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:06:57 ; Search time 3874.81 Seconds

(without alignment)
1431.618 Million cell updates/sec

Title: us-09-019-441-4

Perfect score: 411
Sequence: 1 ATGGAGTTTGCGCTGACGCTG.....TCTGTGTCACCGCTCTCTCA 411

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	69.1	406	9	AM401971 UI-HF-BKO
2	278.4	67.7	613	10	BM007475 603616742
3	277.2	67.4	511	9	AM402613 UI-HF-BKO
4	276	67.2	1164	10	BF974771 602245420
5	275.4	67.0	447	9	AM402793 UI-HF-BKO
6	272.8	66.4	471	9	AM403220 UI-HF-BKO
7	269	65.5	456	9	AM403059 UI-HF-BKO
8	269	65.5	582	9	AM401386 UI-HF-BKO
9	267.8	65.2	443	9	AM401428 UI-HF-BKO
10	266.8	64.9	440	9	AM408304 UI-HF-BKO
11	265.2	64.5	487	9	AM403862 UI-HF-BKO
12	265.2	64.5	740	10	BG757947 602714983
13	265.2	64.5	741	10	BG754024 602709552
14	264.2	64.3	510	9	AM403707 UI-HF-BKO
15	262.4	63.8	908	10	BG686881 602650867
16	262	63.7	879	10	BG759748 602711146
17	261.4	63.6	894	10	BG684839 602636557

18	261.2	63.6	840	10	BG756031 602716521
19	261	63.5	475	9	AM402740 UI-HF-BKO
20	260.8	63.5	587	10	BG684792 602636494
21	260.4	63.4	669	10	BG686716 602650678
22	258.8	63.0	411	9	AM403298 UI-HF-BKO
23	257.8	62.7	390	9	AM631411 hb85d05.Y
24	257.8	62.7	397	9	AM403886 UI-HF-BKO
25	257.2	62.6	735	10	BG745292 602723604
26	257	62.5	613	10	BM007656 603617080
27	256.8	62.5	445	9	AM408316 UI-HF-BKO
28	256.6	62.4	768	10	BM007974 603617710
29	256.4	62.4	770	10	BG758713 602712981
30	255	62.0	491	9	AM402907 UI-HF-BKO
31	254.6	61.9	440	10	BG760171 602733261
32	254.6	61.9	483	9	AM402331 UI-HF-BKO
33	254.2	61.8	390	9	AM408285 UI-HF-BKO
34	254.2	61.8	412	9	AM402895 UI-HF-BKO
35	254	61.8	361	9	AM403412 UI-HF-BKO
36	254	61.8	823	10	BG547512 602574945
37	253	61.6	792	10	BF129047 601811377
38	252.8	61.5	648	10	BG340670 602462250
39	252.6	61.5	705	10	BG758682 602712929
40	252.6	61.5	735	9	AL551886 AL551886
41	251.8	61.3	548	9	AM408295 UI-HF-BKO
42	251.6	61.2	436	9	AM402311 UI-HF-BKO
43	251.4	61.2	372	9	AA581192 m338b11.1
44	250.8	61.0	870	10	BG684039 602635646
45	250.4	60.9	378	9	AA740786 db32e11.s

ALIGNMENTS

RESULT 1
LOCUS AM401971 406 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BKO-aa0-c-04-0-UI.r1 NIH_MGC_36 Homo sapiens CDNA clone
IMAGE:3054342 5', mRNA sequence.

ACCESSION AM401971
VERSION AM401971.1 GI:6920657

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 406)

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgabbs-femail.nih.gov
Bco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbdp/image/image.html

Seq primer: M13 forward

Location/Qualifiers

1. 406
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3054342"

/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"

/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/note="Vector: p77n3-Pac; Site1: NotI; Site2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5440475"
/clone_lib="NH_MGC_113"
/lab_host="DH10B (phage-resistant)"

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/dbdp/IMAGE/image.html
Seq primer: M13 Forward
Location/Qualifiers

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source
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/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/Note="Vector: pTR73-Pac; Site.1: NotI; Site.2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staedt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT      104 a      131 c      151 g      125 t
ORIGIN

Query Match      67.4%; Score 277.2; DB 9; Length 511;
Best Local Similarity 82.6%; Pred. No. 2,7e-66;
Matches 347; Conservative 0; Mismatches 58; Indels 15; Gaps 2;

QY 1 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTCTTTGAAAGGTGCCAGTGGAG 60
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DB 14 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTCTTTGAAAGGTGCCAGTGGAG 73

QY 61 GTGACGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCTGGGGTCCCTGAGACTCTGG 120
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 74 GTGACGCTGGTGGAGTCTGGGGGCGCTTGGTACAGCCTGGAGGCTCCCTGAGACTCTCC 133

QY 121 TGGCAGACCTCCGGGTTTCAGGTTACCTTCAATTACTACTACATGAGCTGGTCCGCGAG 180
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 134 TGTGTAGCCCTCTG-----GATTCACCTTGTAGTATATAAATGAAATGGGTCCGCGAG 187

QY 181 GCTCCAGGAGGGGCGTGGAGTGGGCTCTCAGTATTAGTAGTAGTATGCCACATGCG 240
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 188 GCTCCAGGAGGGGCGTGGAGTGGGCTTTCATCAATTAAGTAGTAGTAGTATGCCACATGCTC 247

QY 241 TAGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCAACACACTG 300
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 248 TAGCAGACTCTGTGAAGGGCGGATTCACCATCTCCAGAGAGAACGCAACACTGCTC 307

QY 301 TTCTCTCAATGAACACCTGAGAGCTGAGAGACAGCGCTGTCTATTACTGTGGAGCTTG 360
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 308 TATCTGCAATGAACACCTGAGAGCGGAGAGACAGCGCTGTATTACTGTGGAGACTC 367

QY 361 ACTAGACAGG-----TCGACTCCTGGGGCCAGGGAGAGTCCGGACCGTCCCTCA 411
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 368 AATAGTGGAGCTACTTTTGTGACTGAGGGCCAGGGAACCTGTGACCGTCTCTCA 427

RESULT 4
BF974771      1164 bp      mRNA      linear      EST 22-JAN-2001
LOCUS         BP974771
DEFINITION    602245420F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336341 5',
                mRNA sequence.
ACCESSION     BF974771
VERSION       BF974771.1
KEYWORDS      GI:12341986
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE     1 (bases 1 to 1164)
AUTHORS      NIH-MGC http://mhc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
                Email: c9apbs-r@mail.nih.gov
                Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
                CDNA Library Preparation: Ling Hong/Rubin Laboratory
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA Sequencing by: Incyte Genomics, Inc.

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FEATURES
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1.1164
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/db_xref="taxon:9606"
/clone_lib="IMAGE:4336541"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: B-cells; Vector: pORF7; Site.1: XhoI;
Site.2: EcoRI; CDNA made by Oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT      284 a      313 c      330 g      236 t      1 others
ORIGIN

Query Match      67.2%; Score 276; DB 10; Length 1164;
Best Local Similarity 82.2%; Pred. No. 7,6e-66;
Matches 350; Conservative 0; Mismatches 55; Indels 21; Gaps 2;

QY 1 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTCTTTGAAAGGTGCCAGTGGAG 60
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DB 64 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTCTTTGAAAGGTGCCAGTGGAG 123

QY 61 GTGACGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCTGGGGTCCCTGAGACTCTGG 120
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 124 GTGACGCTGGTGGAGTCTGGGGGCGCTTGGTACAGCCTGGAGGCTCCCTGAGACTCTCC 183

QY 121 TGGCAGACCTCCGGGTTTCAGGTTACCTTCAATTACTACTACATGAGCTGGTCCGCGAG 180
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 184 TGTGTAGCCCTCTG-----GATTCACCTTGTAGTATATAAATGAAATGGGTCCGCGAG 237

QY 181 GCTCCAGGAGGGGCGTGGAGTGGGCTCTCAGTATTAGTAGTAGTATGCCACATGCG 240
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 238 GCTCCAGGAGGGGCGTGGAGTGGGCTTTCATCAATTAAGTAGTAGTAGTATGCCACATG 297

QY 241 TAGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCAACACACTG 300
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 298 TAGCAGACTCTGTGAAGGGCGGATTCACCATCTCCAGAGAGAACGCAACACTGCTC 357

QY 301 TTCTCTCAATGAACACCTGAGAGCTGAGAGACAGCGCTGTCTATTACTGTGGAG----- 356
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 358 TATCTGCAATGAACACCTGAGAGCGGAGAGACAGCGCGGTCTATTACTGTGGAGAGAT 417

QY 357 -----CTGACTACAGGCTGACTCTGGGGCCAGGAGAGTCTGGTACCGCTC 405
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 418 CAGAGAAACAACAGCTGTAGATTGTGACTACTGGGGCCAGGAGAACCTGTCCACCGCTC 477

QY 406 TCCCTCA 411
DB 478 TCCCTCA 483

RESULT 5
AM402793      447 bp      mRNA      linear      EST 16-FEB-2000
LOCUS         AM402793
DEFINITION    UT-HF-BKO-aag-a-05-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
                IMAGE:3054608 5', mRNA sequence.
ACCESSION     AM402793
VERSION       AM402793.1
KEYWORDS      GI:6921535
SOURCE        human.
ORGANISM      Homo sapiens

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QY	406	TCCTCA	411	
Db	433	TCCTCA	438	
RESULT	7			
LOCUS	AM403059	456 bp	mRNA	linear
DEFINITION	UI-HF-BKO-aal-f-10-0-UI.r1 NIH-MGC-36	Homo sapiens	CDNA clone	EST 16-FEB-2000
IMAGE	3054090 5'			
ACCESSION	AM403059			
VERSION	AM403059.1	GI:6921885		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
AUTHORS	1 (bases 1 to 456)			
TITLE	NIH-MGC http://mgs.nci.nih.gov/			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgsb@remail.nih.gov			
	Eco RI site shown at the beginning of the sequence.			
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
	CDNA Library Preparation: M.B. Soares Lab			
	CDNA Library Arrayed by: M.B. Soares Lab			
	DNA Sequencing by: M.B. Soares Lab			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNC at: www-bio.lnl.gov/bhrp/image/image.html			
	Seq primer: M13 Forward			
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	/tissue_type="lymph"			
	/cell_type="germinal center B cells"			
	/cell_line="MGC85"			
	/lab_host="DH10B (LTI)"			
	/note="Vector: pT73-Pac; Site.1: NotI; Site.2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldi, Ph.D. and M. Bento Soares, Ph.D."			
BASE COUNT	103 a 104 c 139 g 110 t			
ORIGIN				
Query Match	65.5%	Score 269;	DB 9;	Length 456;
Best Local Similarity	83.9%	Pred. No. 4.9e-64;		
Matches 318:	Conservative 0;	Mismatches 55;	Indels 6;	Gaps 1;
QY	1	ATGGAGTTGGGCTAGAGTGGGGTTTCCCTGTTCTCTTTGAAGGTGCAGTGTGAG	60	
Db	52	ATGGAGTTGGGGCTGTGCTGGGTTTCTTGTGCTATTATTTAGAAAGGTGCAGTGTGAG	111	
QY	61	GTCAGCTGTGTGACTGTGGGGGGCGCTTGGCAAGACCTGGGGGGTCCCTGAGACTTCG	120	
Db	112	GTCAGCTGTGTGAGTGTGGGGGAGCTTGGTACAGCCTGGAGGGTCCCTGAGACTTCG	171	
QY	121	TGCGAGGCTCCGGGTTACAGTTACCTTCATATCTACTACATGGAGTGGTCCGCCAG	180	
Db	172	TGTGAGGCTCTG-----GATTCACCTTCAGTAGTATTGGAATGAACCTGGGTCGCCAG	225	
QY	181	GCTCCAGGGGAGGGGCTGGAGTGTCTACACATTATTAAGTAGAGTGTGATCCACATCG	240	
Db	226	GCTCCAGGGGAGGGGCTGGAGTGTGTTCATCATATTAGTAGTAGTAGTACCATATAC	285	
QY	241	TACGCAAGATCCGTAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACTCG	300	

Db	286	TACGAGACTCTGTGAAGGGCCGATTCACCAATTCTCAGACAAACCGACAGACTCATG	345
Oy	301	TTTCTTCAATGACACAGCCTCAGAGCTTAGACACACGCCTGTCATTAATCTAGTCGACCTTG	360
Db	346	TATCTGCCAAAGAAGAGGCTCAGAGCCAGACGAGCAGCAGCTGTTATTAATCTAGTCGCGGCAT	405
Oy	361	ACTACAGGCTCTGACCTCT	379
Db	406	ATAGCAGCAGCTGACGACT	424
RESULT	8		
LOCUS	AM401386	582 bp mRNA linear EST 16-FEB-2000	
DEFINITION	UT-HF-BK0-zau-b-03-0-U1.r1 NIH_MGC_36 Homo sapiens cDNA clone		
ACCESSION	AM401386		
VERSION	AM401386.1	GI:6920168	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D. CDNA Library Arrayed by: M.B. Soares Lab DNA sequencing by: M.B. Soares Lab clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at: www.bio.llnl.gov/dbfp/image/image.html Seq primer: M13 Forward.		
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	/clone_id="NIH_MGC_36"		
	/tissue_type="lymph"		
	/cell_type="germinal center B cells"		
	/cell_line="MGC85"		
	/lab_host="DH10B (LTI)"		
	/note="Vector: pTZ19-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonafido, Ph.D. and M. Bento Soares, Ph.D."		
BASE COUNT	117 a 155 c 169 g 141 t		
ORIGIN			
Query Match	65.5%; Score 269; DB 9; Length 582;		
Best Local Similarity	81.5%; Pred. No. 5.3e-64;		
Matches 340; Conservative	0; Mismatches 65; Indels 12; Gaps 2;		
Oy	1	ATGAGCTTTGGGCGTAGCTGGGGGCTTTCCTGTGCTCTTTTGAAGGCGTCCAGTGTGAG	60
Db	75	ATGGAGTTGGGGCTGTGCTGGGTTTCCTGTGCTATTTTAGAAGGTCCTATGTGAA	134
Oy	61	GTCGAGCTGTGAGACTGGGGGCGGCTTGGCAAAGCCGTGGGGGCTCCCTGAGACTCTG	120
Db	135	GAACATCTGTGAGACTGGGGGACCCTTGGTACAGCCTGGAGGGTCCCTGAGACTCTCC	194
Oy	121	TGCGAGGCTCCGGGTTAGGTTCACTCACTTAATACCTACTACTAGACTGGGTCCGCCAG	180
Db	195	TGTGAGGCTCTG-----GATTACCTTCAGTGTATGAAATTGAACTGGGTCGCCAG	248

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library.

BASE COUNT
 ORIGIN

166 a 203 c 206 g 165 t

Query Match 64.5%; Score 265.2; DB 10; Length 740;
 Best Local Similarity 86.2%; Pred. No. 6.5e-63;
 Matches 307; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 1 ATGAGTTGGGCTGAGCTGGGTTTCCTTCTCTTTGAAAGGTGTCAGTGAG 60
 Db ATGAGTTGGGCTGAGCTGGGTTTCCTTCTCTTTGAAAGGTGTCAGTGAG 83
 QY 61 GTGAGCTGTGTGAGTCTGGGGGCGGCTTGCAAGCCTGGGGGCTCCCTGAGACTCTGG 120
 Db GTGAGCTGTGTGAGTCTGGGGGCGGCTTGCAAGCCTGGGGGCTCCCTGAGACTCTCC 143
 QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACCTTCATTAATTAATTAATGAGTGGGTCGCCAG 180
 Db TGTGACACCTCTCTG-----GATTCACCTTCAGTAGTATACATGAACTGGTCCGCCAG 197
 QY 181 GCTCAGGCGGAGGGGCTGAGATGGGTTCTCACGTTAGTACTAGTGGATCCACATGG 240
 Db GCTCAGGCGGAGGGGCTGAGATGGGTTCTCACGTTAGTACTAGTGGATCCACATGAC 257
 QY 241 TACGACACTCCGTAAGAGGCGAGATTACATCTCCAGAGAGAGCAACCAACACACTG 300
 Db TACGACACTCTGTGAAGGGCGGATTCACCATCTCCAGAGAGCAATGCCAAGAACTCACTG 317
 QY 301 TTCTTCAATGAACACCTGAGAGCTGAGAGACAGGCGTGTCTATTACTGTGGCAG 356
 Db TATCTGCAAAATGAACACCTGAGAGAGAGAGACAGGCGTGTCTATTACTGTGGCAG 373

RESULT 13

LOCUS

BC754024 741 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602709552F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846117 5',
 mRNA sequence.

ACCESSION BC754024
 VERSION BC754024.1 GI:14064677
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 741)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)

REFERENCE Unpublished (1999)
 AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE Email: cgabs-r@mail.nih.gov
 JOURNAL Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 COMMENT CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LCM1686 row: g column: 14
 High quality sequence stop: 735.

FEATURES
 source location/Qualifiers

1. 741
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4846117"
 /clone_lib="NIH_MGC_48"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pORF7; Site:1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(C). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library.

BASE COUNT 166 a 204 c 206 g 165 t
 ORIGIN

Query Match 64.5%; Score 265.2; DB 10; Length 741;
 Best Local Similarity 86.2%; Pred. No. 6.5e-63;
 Matches 307; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 1 ATGAGTTGGGCTGAGCTGGGTTTCCTTCTCTTTGAAAGGTGTCAGTGAG 60
 Db ATGAGTTGGGCTGAGCTGGGTTTCCTTCTCTTTGAAAGGTGTCAGTGAG 83
 QY 61 GTGAGCTGTGTGAGTCTGGGGGCGGCTTGCAAGCCTGGGGGCTCCCTGAGACTCTGG 120
 Db GTGAGCTGTGTGAGTCTGGGGGCGGCTTGCAAGCCTGGGGGCTCCCTGAGACTCTCC 143
 QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACCTTCATTAATTAATTAATGAGTGGGTCGCCAG 180
 Db TGTGACACCTCTCTG-----GATTCACCTTCAGTAGTATACATGAACTGGTCCGCCAG 197
 QY 181 GCTCAGGCGGAGGGGCTGAGATGGGTTCTCACGTTAGTACTAGTGGATCCACATGG 240
 Db GCTCAGGCGGAGGGGCTGAGATGGGTTCTCACGTTAGTACTAGTGGATCCACATGAC 257
 QY 241 TACGACACTCCGTAAGAGGCGAGATTACATCTCCAGAGAGAGCAACCAACACACTG 300
 Db TACGACACTCTGTGAAGGGCGGATTCACCATCTCCAGAGAGCAATGCCAAGAACTCACTG 317
 QY 301 TTCTTCAATGAACACCTGAGAGCTGAGAGACAGGCGTGTCTATTACTGTGGCAG 356
 Db TATCTGCAAAATGAACACCTGAGAGAGAGAGACAGGCGTGTCTATTACTGTGGCAG 373

RESULT 14

LOCUS AM403707 510 bp mRNA linear EST 16-FEB-2000
 DEFINITION UT-HF-BKO-abh-f-08-0-UT-RT NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3056391 5', mRNA sequence.

ACCESSION AM403707
 VERSION AM403707.1 GI:6922724
 KEYWORDS EST.

SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 510)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)

REFERENCE Unpublished (1999)
 AUTHORS Contact: Robert Strausberg, Ph.D.
 TITLE Email: cgabs-r@mail.nih.gov
 JOURNAL Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 COMMENT CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.llnl.gov/bdrp/image/image.html
 Seq primer: M13 forward

FEATURES
 source location/Qualifiers

1. 510
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3056391"
 /clone_lib="NIH_MGC_36"

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:58:50 ; Search time 488.47 Seconds

(without alignments)
1444.617 Million cell updates/sec

Title: us-09-019-441-4

Perfect score: 411
Sequence: 1 ATGGAGTTTGGCGTACGCTG.....TCTGCTGTCACGCTCTCTCA 411

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
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- 19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	411	100.0	411	19	AAV33310	Anti-human CD23 5E
2	369.4	89.9	19035	19	AAV61794	Traget Plasmid Man
3	293	71.3	458	22	AAH41153	Human coding seque
4	282.6	68.8	1710	22	AA522533	Human CDNA encodin
5	282.6	68.8	1721	22	AA522530	Human CDNA encodin
6	267.4	65.1	19	AAV24243	Chimeric antibody	
7	267.4	65.1	411	20	AAZ00116	Human antibody hea
8	267.4	65.1	411	21	AA258914	DNA seq ID No: 58.
9	267.4	65.1	411	22	AAH75115	Nucleotide sequenc

10	267.4	65.1	411	22	AAH74285	Nucleotide sequenc
11	267.4	65.1	411	22	AAH76645	Humanised anti-PTH
12	267.4	65.1	411	22	AAH69130	Human antibody H c
13	267.4	65.1	411	22	AAH69186	Human antibody H c
14	267.4	65.1	411	22	AAH69242	Human antibody H c
15	266	64.7	1458	22	AA522625	Human CDNA encodin
16	262.2	63.8	1983	22	AAH98583	Human CDNA encodin
17	261.6	63.6	1741	22	AA522531	Human EST-derived
18	261.2	63.6	1366	22	AAH98760	Human EST-derived
19	261	63.5	456	11	AAO03610	Sequence encoding
20	260	63.3	1736	22	AA522532	Human CDNA encodin
21	259.6	63.2	1427	19	AAV41431	Plasmid Hu19CHPCD
22	258.2	62.8	432	15	AAO71717	Monoclonal antibod
23	258	62.8	1427	19	AAV41432	Plasmid Hu19BPCD
24	258	62.8	1427	19	AAV41432	Plasmid Hu19BPCD
25	256.8	62.5	637	23	AA591077	DNA encoding novel
26	256.6	62.4	445	18	AA772237	Humanised reshaped
27	254.6	61.9	1392	21	AAA46864	DNA encoding the h
28	254.6	61.9	1392	21	AAA46890	DNA encoding the h
29	254.6	61.9	1392	21	AAA46892	DNA encoding the h
30	254.6	61.9	1999	21	AAA46891	DNA encoding the h
31	253.2	61.6	1395	21	AAA46866	DNA encoding the h
32	253.2	61.6	1395	21	AAA46894	DNA encoding the h
33	252.6	61.5	1392	21	AAA46870	DNA encoding the h
34	252.6	61.5	1392	21	AAA46896	DNA encoding the h
35	252.2	61.4	393	17	AAH46130	Monoclonal antibod
36	252.2	61.4	393	18	AAH85839	Monoclonal antibod
37	252	61.3	1651	21	AAH15694	Cancer suppressor
38	252	61.3	1651	22	AAO07360	Human DNA encoding
39	251.8	61.3	483	13	AAO31888	CLN-IgG gamma. Sy
40	251.8	61.3	483	15	AAO64065	Anti-cancer monoc
41	251.4	61.2	411	20	AA622787	Human anti-ganglio
42	251.2	61.1	761	20	AAH01214	Human antiFc epsil
43	250.8	61.0	1605	22	AAH18432	Human CDNA sequenc
44	250.6	61.0	393	15	AAO64051	Sequence of the VH
45	247.6	60.2	1951	24	AA562797	CDNA sequence #584

ALIGNMENTS

RESULT	1
AAV33310	
ID	AAV33310 standard; DNA: 411 BP.
XX	
AC	AAV33310;
XX	
DT	18-NOV-1998 (first entry)
XX	
DE	Anti-human CD23 5E8 monoclonal antibody heavy chain variable region DNA.
XX	
KW	Anti-human CD23 5E8 monoclonal antibody; heavy chain variable region;
KW	human CD23; IGE: FcεR1/CD23; gamma-1 constant region;
KW	gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW	allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
XX	
OS	Macaca fascicularis
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..411
FT	/tag a "anti-human CD23 5E8 heavy chain variable
FT	/product- "region"
FT	/note- "CDS does not contain a stop codon"
FT	1..57
FT	sig_peptide
FT	/tag- b
FT	mat_peptide
FT	58..411
FT	/tag c
FT	misc_feature
FT	148..168
FT	/tag d
FT	/note- "encodes CDR 1 region"
FT	211..261
FT	misc_feature
FT	/tag e

```

FT      /note= "encodes CDR 2 region"
FT      misc_feature 358..378
FT      /*tag= f
FT      /note= "encodes CDR 2 region"
XX      WO9837099-A1.
XX      27-AUG-1998.
XX      17-FEB-1998; 98MO-US02253.
XX      05-FEB-1998; 98US-0803085.
XX      20-FEB-1997; 97US-0803085.
XX      (IDEC-) IDEC PHARM CORP.
XX      (SEK ) SEIKAGAKU CORP.
XX      Kioetzer WS, Nakamura T, Ref ME;
XX      WPI; 1998-467495/40.
XX      P-PSDB; AAW70380.
XX      New anti-human CD23 monoclonal antibody - used for inhibiting Ige
XX      expression to treat or prevent allergic, inflammatory and
XX      auto-immune conditions
XX      Example 1: Pages 108-110; 146pp; English.
XX      The present sequence represents a DNA sequence encoding the heavy
XX      chain variable region of primate monoclonal antibody anti-human CD23 5E8.
XX      The invention provides primate monoclonal antibodies which specifically
XX      bind human CD23, the low affinity receptor for Ige (FcεRI/CD23),
XX      and comprise either of a human gamma-1 or human gamma-3 constant region
XX      that binds to human Fc gamma receptors and inhibits Ige expression.
XX      The monoclonal antibodies of the invention are claimed to be useful
XX      for inhibiting induced Ige production for treating or preventing
XX      allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX      conjunctivitis, autoimmune haemolytic anaemia, etc.
XX      Sequence 411 BP; 80 A; 102 C; 130 G; 99 T; 0 other;
SQ
Query Match 100.0%; Score 411; DB 19; Length 411;
Best Local Similarity 100.0%; Pred. NO. 1e-106;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGATTGGGCTGAGCTGGGTTTCTGTTCTGTTGAAAGGTGTCAGTGTGAG 60
    |||||||
DB 1 atggaatttggtcgtgagctggtttctctctctttgaaaggtgtccagtgag 60
QY 61 GTGACGTGGTGGAGTGTGGGGGCGCTTGCAAGCCTGGGGGTCCTGAGACTGTGG 120
    |||||||
DB 61 gtgcaagctgtgtgagctgtggtggtgcaagcctgtggtgtccctgagactctg 120
QY 121 TGGCAGCTCTCCGGGTCAGGTTCACTTCAATTAAGTACATGAGACTGGTCCGGCAG 180
    |||||||
DB 121 tgcgaagctccgggtgtcgaagttcaactcaataacacacagagctggtccgcaag 180
QY 181 GCTTCAGGAGGAGGGCTGAGTGGGTCTCAAGTATTAGTAGTAGTGATCCACATGCG 240
    |||||||
DB 181 gcttcagagaggggtcgtgagtggtctcaagtattagtagtggtgtgtccacatg 240
QY 241 TAGCAGACTTCCTGGAAGGCGCATTCACCATCTCCAGAGAGAAAGCGCAACACACTG 300
    |||||||
DB 241 tagcagacttcctgtgaagggcagaattcacacatccagagagaagcacaacacactg 300
QY 301 TTCTTCAATGAAACACCTGAGAGCTGAGAGACAGGCTGTCTTACTGTGCGAGCTTG 360
    |||||||
DB 301 ttcttcaaatgaacacacctgagagctgagagacagcgtgtctattactgtgcagcttg 360
QY 361 ACTACAGGCTGTGACTCTGTGGGCGCAGAGAGTCTGTGTCACCGTCTCTCA 411
    |||||||
DB 361 actacaggtgtgactctgtgggccaaggtctctgtgtcacctctctctca 411

```

```

RESULT 2
ID AAV61794
XX AAV61794 standard; DNA; 19035 BP.
XX AAV61794;
XX 07-JUN-1999 (first entry)
DE Target plasmid Mandy containing anti-CD23 gene.
XX Mandy; target plasmid; gene integration; gene amplification;
XX homologous recombination; vector; neomycin phosphotransferase;
XX neo gene; selectable marker; immunoglobulin; CD23; 5E8; human; ss.
XX
OS Chimeric - Mus sp.
OS Chimeric - Escherichia coli.
OS Chimeric - Baculovirus.
OS Chimeric - Cytomegalovirus.
OS Chimeric - Rhesus macaque polyoma virus.
OS Chimeric - Photinus sp.
OS Chimeric - Salmonella typhimurium.
OS Chimeric - Homo sapiens.
XX
FH key
FH Location/Qualifiers
FT 361
FT misc_feature
FT /*tag=
FT /note=
FT "this base represents a nucleotide missing
    from the sequence given in the
    specification. It is included to
    maintain the nucleotide numbering in the
    specification for this sequence"
FT 721
FT misc_feature
FT /*tag=
FT /note=
FT "this base represents a nucleotide missing
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    maintain the nucleotide numbering in the
    specification for this sequence"
FT 2941
FT misc_feature
FT /*tag=
FT /note=
FT "this base represents a nucleotide missing
    from the sequence given in the
    specification. It is included to
    maintain the nucleotide numbering in the
    specification for this sequence"
FT 3301
FT misc_feature
FT /*tag=
FT /note=
FT "this base represents a nucleotide missing
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    maintain the nucleotide numbering in the
    specification for this sequence"
FT 4261
FT misc_feature
FT /*tag=
FT /note=
FT "this base represents a nucleotide missing
    from the sequence given in the
    specification. It is included to
    maintain the nucleotide numbering in the
    specification for this sequence"
FT 4621..4622
FT misc_feature
FT /*tag=
FT /note=
FT "these bases represent nucleotides missing
    from the sequence given in the
    specification. They are included to
    maintain the nucleotide numbering in the
    specification for this sequence"
FT 8161
FT misc_feature
FT /*tag=
FT /note=
FT "this base represents a nucleotide missing
    from the sequence given in the
    specification. It is included to
    maintain the nucleotide numbering in the
    specification for this sequence"
FT

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Db 9672 tacgcagaccctgtaaggcgagattaccatctccagagagaacccaagaacacactg 9731

QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360

Db 9732 ttcttcaaatgaacagccctgagagctgagagacacggtctctattactgctgagcttg 9791

QY 361 ACTACAGGGTCTGACTCTCTGGGCGCCAGGGAGTCTCTGTCTACCGCTCTCTCTCA 411

Db 9792 actacagggctgactcctctgggcccaggagctcctggttcacccgtctctctca 9842

RESULT 3

AH41153

ID AAH41153 standard; DNA; 458 BP.

XX

AC AAH41153;

XX

DT 22-AUG-2001 (first entry)

DE Human coding sequence SEQ ID 3.

XX

KW Human: antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;

KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;

KW signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.

XX

OS Homo sapiens.

XX

PN WO200136642-A1.

XX

PD 25-MAY-2001.

XX

PF 17-NOV-2000; 2000WO-JP08129.

XX

PR 18-NOV-1999; 99JP-0328681.

PR 08-NOV-2000; 2000JP-0340216.

XX

PA (NISR) JAPAN TOBACCO INC.

XX

PI Sakamoto S, Kamada M;

XX

DR WPI; 2001-343825/36.

DR P-PSDB; AAB99111.

XX

PT Human monoclonal antibodies recognizing human TGF-beta II receptor,

PT useful for treating TGF-beta associated diseases such as tissue

PT fibrosis

XX

PS Example 12; Page 94-95; 118pp; Japanese.

XX

CC The present invention relates to novel human monoclonal antibodies. The

CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II

CC receptor, resulting in the inhibition of the signal transduction of human

CC TGF-beta into cells. The antibodies can be used for the prevention and

CC treatment of diseases associated with the production of TGF-beta, such as

CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,

CC atherosclerosis, atopy, keloid and arthritis. The present sequence was

CC used in the present invention.

XX

Sequence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;

QY 1 ATGAGCTTTGGGCTGAGCTGGGCTTTCTCTGTTCTCTTTTGAAGGTGTCAGTGTGAG 60

Db 1 atggaactggggctccgcgtgggttctctgttctgttctatttagaagggtccagtgtag 60

QY 61 GTCAGCTGTGAGTCTGGGGCGGCTTGGCAAGCTGGGGGCTCCCTGAGACTCTGG 120

Db 61 gtcaactggtgagtgctggggagggccctggttcaggccttgggggtccctgagactctcc 120

QY 121 TGGCAGCCTCGGTTTCAGGTTTCACTTCAATAACTACTACATGGACTGGTCCGCCAG 180

Db 121 tgtgcagcctctg-----gattcacctctcagtagctttagcagtaactggtgccgacg 174

QY 181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTACGCTATTAGTAGTAGTGTGATGCCACATGG 240

Db 175 gtccagggaagggtggtgagtggtctcatccattagtagtagtagtagttacatatac 234

QY 241 TAGCGAGACTCCGCTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300

Db 235 tacacagactcagtgaaaggccagattcaccatctccagagacaacgccagaactcactg 294

QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGCTGTCTATTACTGTGCGAGCTTG 360

Db 295 tatctgcaaatgaacagcctgagagcgagacacagcgtgtattactgtgtagagagg 354

QY 361 ACTACAGGCTCTGACTCTCTGGGCGCCAGGGAGTCTCTGGTCACTCTCTCTCA 411

Db 355 tactgggggttgactactggggccagggaacctgtcacccgtctctctca 405

RESULT 4

AAS22533

ID AAS22533 standard; cDNA; 1710 BP.

XX

AC AAS22533;

XX

DT 24-OCT-2001 (first entry)

DE Human cDNA encoding a novel human protein #99.

XX

KW Human: novel protein; ss; Antianaemic; osteopathic; antiinflammatory;

KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;

KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;

KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;

KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;

KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;

KW tissue regeneration; immune disorder.

OS Homo sapiens.

XX

PN WO200155437-A2.

XX

PD 02-AUG-2001.

XX

PF 25-JAN-2001; 2001WO-US02623.

XX

PR 25-JAN-2000; 2000US-0491404.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-451939/48.

DR P-PSDB; AAU14228.

XX

PT Isolated polypeptides useful for treating anti-inflammatory diseases,

PT nervous system disorders, and for regenerating bone and cartilage -

XX

PS Claim 1; Page 306-308; 894pp; English.

XX

CC The invention relates to polynucleotides encoding novel human

CC proteins or their active domains. The polypeptides, polynucleotides and

CC antibodies raised against the polypeptides are used in a method of

CC treatment of a mammal and prevention of disorders caused by the aberrant

CC protein expression or activity. The polypeptides can be used as

CC molecular weight markers, food supplements, and in antibody production.

CC The polypeptides are used to identify compounds which bind to the

CC polypeptides. Polynucleotides of the invention are used as probes and

CC primers, for sequencing, for chromosome or gene mapping, in the

CC production of recombinant proteins, and in generating anti-sense DNA or

CC RNA and in gene therapy. Polypeptides of the invention can be used to

CC target drugs to a tumour. In assays to determine biological activity, to


```
FT CDS 1..411
FT /*tag= a
FT sig_peptide 1..57
FT /*tag= b
FT mat_peptide 58..411
FT /*tag= c
XX WO200164249-A1.
XX 07-SEP-2001.
XX 30-AUG-2000; 2000WO-JP05986.
XX 28-FEB-2000; 2000JP-0052414.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX Saito H, Tsunenari T, Onuma E, Sato K;
XX WPI; 2001-550131/61.
XX P-PSDB; AAG67112.
XX Tissue decomposition inhibitor that prevents parathyroid hormone
XX associated proteins from binding to its receptor
XX Example 1; Page 107-108; 132pp; Japanese.
XX The specification describes a tissue decomposition inhibitor, which
XX comprises a substance that inhibits peptides associated with
XX parathyroid hormone (PTH) from binding with their receptor. The method
XX is used to inhibit tissue decomposition caused by cancer cachexia,
XX septicemia, heavy external injury or muscular dystrophy, and for
XX treating patients with elevated cytokine (Interleukin-6, Granulocyte
XX colony stimulating factor, Interleukin-11 and Leukemia inhibitory
XX factor) levels. It may also be used for preventing weight loss caused
XX by cancer cachexia. The present sequence encodes a protein, which is
XX used in the course of the invention.
XX Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
```

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Query Match 65.1%; Score 267.4; DB 22; Length 411;
Best Local Similarity 81.3%; Pred. No. 4.5e-66;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTTCCCTTTTGAAGGTGCCAGTGTGAG 60
Db 1 atggggttgggctgagctgggttttccctgttgccttttaagagggtccagtgctcag 60

QY 61 GTCAGCTGTGTGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgtgagctgtggggagcggtgtccagcctgggaggtccctgagactctcc 120

QY 121 TGGCGACGCTCCGGGTTACGTTTCACTTCAATACTACTACATGAGCTGGGTCCGCCAG 180
Db 121 tgtcagcctctg-----gattcaactcagtagctatggcattcttgggtccgcccag 174

QY 181 GTCACAGGGCAGGGCTGAGTGGGTCTACGTTATTAGTAGTGTGATCCACATGG 240
Db 175 gctccaggcaagggtgagtggtggcaaccattagtagtggtgtagttacacctac 234

QY 241 TAGCGAGTCTCCGTGAAGGCGAGATTACACATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 tatccagacagtgtgaaggggcgattccacatctccagagacaattcccaagaacacgctg 294

QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 295 tatctgcaaatgaacagcctgagagctgagagacagcgctgtgtattactgtgagacag 354

QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCCAGGGAGTCTGTGTCACCGTCTCTCTCA 411
Db 355 actactatgacttacttcttacttggggccagggaaccttggtcaccgtctctctca 411
```

```
RESULT 10
AAH74285
ID AAH74285 standard; DNA; 411 BP.
XX
AC AAH74285;
XX 15-OCT-2001 (first entry)
XX Nucleotide sequence of a human polypeptide.
XX Parathyroid hormone-associated peptide; PTHrP; dental disease; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..411
XX /*tag= a
XX /*note= "no termination codon given"
XX mat_peptide 58..411
XX /*tag= b
XX WO200154725-A1.
XX 02-AUG-2001.
XX 14-DEC-2000; 2000WO-JP08875.
XX 25-JAN-2000; 2000JP-0083034.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX Kato A, Suzuki M, Sugimoto T;
XX WPI; 2001-465459/50.
XX P-PSDB; AAG63394.
XX Parathyroid hormone-associated peptide binding inhibitors useful for
XX treating dental disease
XX Disclosure; Page 113-114; 140pp; Japanese.
XX The specification describes a treatment for dental diseases. The
XX treatment comprises a substance that inhibits binding between
XX parathyroid hormone-associated peptide and its receptor. The
XX present sequence encodes a human protein, which is used in the
XX course of the invention.
XX Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
```

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Query Match 65.1%; Score 267.4; DB 22; Length 411;
Best Local Similarity 81.3%; Pred. No. 4.5e-66;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTTCCCTTTTGAAGGTGCCAGTGTGAG 60
Db 1 atggggttgggctgagctgggttttccctgttgccttttaagagggtccagtgctcag 60

QY 61 GTCAGCTGTGTGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgtgagctgtggggagcggtgtccagcctgggaggtccctgagactctcc 120

QY 121 TGGCGACGCTCCGGGTTACGTTTCACTTCAATACTACTACATGAGCTGGGTCCGCCAG 180
Db 121 tgtcagcctctg-----gattcaactcagtagctatggcattcttgggtccgcccag 174

QY 181 GTCACAGGGCAGGGCTGAGTGGGTCTACGTTATTAGTAGTGTGATCCACATGG 240
Db 175 gctccaggcaagggtgagtggtggcaaccattagtagtggtgtagttacacctac 234

QY 241 TAGCGAGTCTCCGTGAAGGCGAGATTACACATCTCCAGAGAGAACGCCAACACACTG 300
Db 241 tatccagacagtgtgaaggggcgattccacatctccagagacaattcccaagaacacgctg 300
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Db 235 tatccagacagtgtgaaggcgattccaccatctccagagacaattccaaagaacacgctg 294
 QY 301 TTTCCTCAATGAACAGCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGAGCTTG 360
 Db 295 tatctgcaaatgaacagcctgagagctgagacacgctgtgtattactgtgcgagacag 354
 QY 361 ACTACAGGCTCTAC-----TCCTGGGCGCCAGGAGTCTGTGTCACCGTCTCTCA 411
 Db 355 actactatgactacttcttacttggggccaggggaacccctggtccaccgtctccctca 411

RESULT 11
 AAH76645
 ID AAH76645 standard; DNA; 411 BP.
 XX
 AC AAH76645;
 XX
 DT 08-OCT-2001 (first entry)
 XX
 DE Humanised anti-PTHrP Ab heavy chain version a DNA, SEQ ID NO:58.
 XX
 KW Parathyroid hormone-related peptide; PTHrP; antagonist; antibody;
 KW calcium regulation disorder; serum calcium concentration; heavy chain;
 KW humoral hypercalcaemia of malignancy; cytostatic; analgesic; humanised;
 KW ds.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 CDS 1..411
 FT /*tag- a
 FT /partial
 FT /product= "Heavy chain precursor"
 FT /note= "No stop codon given in the specification"
 FT sig_peptide 1..57
 FT /*tag= b
 FT mat_peptide 58..411
 FT /*tag= c
 FT /product= "Mature heavy chain"
 XX
 WO200147554-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 27-DEC-2000; 2000WO-JP09339.
 XX
 PR 28-DEC-1999; 99JP-0375203.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Yamazaki T, Hayasaka A, Koga A;
 XX
 DR WPI; 2001-425590/45.
 DR P-PSDB; AAG64774, AAG64776.
 XX
 PT Composition for treating diseases of calcium regulation and for use as
 PT an analgesic, comprises an antibody recognizing parathyroid hormone
 PT related peptide
 XX
 PS Examples; Page 105-106; 128pp; Japanese.
 XX
 CC The invention relates to a stabilised composition of an antibody which
 CC recognises parathyroid hormone-related peptide (PTHrP) - see AAG64793.
 CC The composition consists of a solution of the antibody in a buffer of pH
 CC 5-8 containing one or more of acetic acid, phosphoric acid, citric acid
 CC and their salts. The composition has increased storage stability,
 CC especially at elevated temperatures. The composition antagonises the
 CC action of PTHrP, and may be used in the treatment of diseases involving
 CC disturbances of calcium regulation (high or low serum calcium
 CC concentration) such as humoral hypercalcaemia of malignancy and as an
 CC analgesic. The present sequence represents DNA encoding a humanised

CC version of the heavy chain of anti-human PTHrP murine monoclonal antibody
 CC 23-57-137-1.
 XX
 SQ Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
 Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

Query Match 65.1%; Score 267.4; DB 22; Length 411;
 Best Local Similarity 81.3%; Pred. No. 4.5e-66;
 Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTTTCCTTTTAAAGGTGTCCAGTGTGAG 60
 Db 1 atggggtttgggctgagctgggttttccctcgcttctttaagaggtgtccagtgca 60
 QY 61 GTGCAGCTGGTGGAGTCTGGGGCGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120
 Db 61 gtgcagctggtggagtctgggggagcggtgtccagcctgggaggtccctgagactctcc 120
 QY 121 TGGCAGAGCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGGGTCGCCCGAG 180
 Db 121 tggcagagcctcg-----gattcaccttcagtagctatggcatgtcttgggtccgcca 174
 QY 181 GTCCAGGCGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGTGATCCACATGG 240
 Db 175 gctccaggaagggtgagtggtggcaaccattagtagtggtgtgttagttacacctac 234
 QY 241 TAGCAGACTCCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
 Db 235 tatccagacagtgtgaagggtgattcacctctccagagacaattccaagaacacgctg 294
 QY 301 TTTCCTCAATGAACAGCTGAGAGCTGAGGACCGCTCTCTATTACTGTGCGAGCTTG 360
 Db 295 tatctgcaaatgaacagcctgagagctgagacacgctgtgtattactgtgcgagacag 354
 QY 361 ACTACAGGCTCTAC-----TCCTGGGCGCCAGGAGTCTGTGTCACCGTCTCTCA 411
 Db 355 actactatgactacttcttacttcttactggggccagggaaacctggtccacctctctca 411

RESULT 12
 AAH769130
 ID AAH769130 standard; DNA; 411 BP.
 XX
 AC AAH769130;
 XX
 DT 12-APR-2001 (first entry)
 XX
 DE Human antibody H chain protein SEQ ID NO:58.
 XX
 KW Human; mouse; parathyroid hormone-related peptide; PTHrP; vasopressin;
 KW monoclonal antibody; antidiarrheic; antiemetic; antidiabetic;
 KW antipyretic; cancer; dehydration; excessive urination; thirst;
 KW vomiting; diarrhoea; fever; perspiration; diabetes; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200102010-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 03-JUL-2000; 2000WO-JP04413.
 XX
 PR 02-JUL-1999; 99JP-0189322.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Ogata E, Onuma E, Tsunenari T, Saito H, Azuma Y;
 XX
 DR WPI; 2001-112507/12.
 XX
 PT Inhibitor of parathyroid hormone related peptide binding to its
 PT receptor can ameliorate symptoms caused by a decrease in vasopressin
 PT level due to cancer

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XX Example 2; Page 90-91; 114pp; Japanese.
PS
XX The present invention describes an agent (I) for ameliorating low
CC vasopressin levels, and symptoms caused by this depression, containing
CC as an active component a substance which inhibits the binding of
CC parathyroid hormone related peptide (PTHrP) to its receptor. (I) has
CC antidiarrhetic, antiemetic, antidiabetic and antipyretic activities.
CC (I) can be used for the amelioration of symptoms caused by decrease in
CC vasopressin levels, such as that due to cancer are treated using the
CC agent. These symptoms include dehydration, excessive urination, thirst,
CC vomiting, diarrhoea, fever, perspiration and diabetes. AAF69085 to
CC AAF69140 and AAB76879 to AAB76897 represent sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;

Query Match      65.1%; Score 267.4; DB 22; Length 411;
Best Local Similarity 81.3%; Pred. No. 4.5e-66;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGCGTGACGTGGGTTTTTCCTTTCTCCTTTTGAAGAGTGTCAGTGATGG 60
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atggggtttggcgtagctgggttttccctgttgctctttaaggagtgtccagtgtcag 60

QY 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 gtgcagctgttgagtcgtgggagcggtgtgccagcctgggaggtgccctgagactctc 120

QY 121 TGCGACGCCCTCGGGTTCAGGCTTCACCCTTCAATAAACPACTACATGGACTGGTGGTCCGCGCAG 180
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 tgtgcagcctctg-----gattcacctcagtagctatggcatgtcttgtgggtccgcag 174

QY 181 GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGATTATTAATAGTAGTAGTGTGATGCCACATGG 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 gctccaggcaagggtgtgagtggtgtgacaccattagtagtggtgtgtagttacacctac 234

QY 241 TACGCACACTCCGTGAAGGCGCATTCACCATCTCCACAGAGAGAAGCGCCAACAACACACTG 300
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 235 tatccagaacagtgtgaagggtgggatccaccatctcccagagacaattccagaacacagctg 294

QY 301 TTCTTCAAATGAACACGCTGAGAGCTGAGGACACGCGCTCTCTATTACTGTGCGAGCTTG 360
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 295 tatctgcaaatgaacagcctgagagctgaggacagcggtgtgtattactgtgcgagacag 354

QY 361 ACTACAGGGCTCAC-----TCTGGGGCCAGGAGTCTGCTGCTACCGTCTCCTCA 411
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 actactatgacttacttctgcttactggttactgggccaaggaaacctgtgcaccgtctctcca 411

RESULT 13
AAF69186
ID AAF69186 standard; DNA; 411 BP.
XX
AC AAF69186;
XX
DT DT
DE DE
DE DE
KW Human; mouse; hypercalcaemia; parathyroid hormone; PTH; PTHrP;
KW parathyroid hormone related peptide; analgesic; immunosuppressive;
KW nootropic; neuroprotective; antiinflammatory; cytosstatic; antithyroid;
KW eating-disorder; cardiovascular; pain; immune suppression; appetite;
KW digestive system; protein metabolism; sugar metabolism; lipid metabolism;
KW blood chemistry; thyroid function; electrolyte balance; neurological;
KW central nervous system disorder; sleep disturbance; brain function;
KW brain circulation; autonomic nervous system; blood poisoning; dropsy;
KW inflammation; blood disease; calcium disturbance; autoimmune disease; ds.
XX
XX Homo sapiens.
XX

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Db	295	tatctgcaaatgacacgctgagagctgaggacacgagctgtgtattattctgtgagacag	354
Qy	361	ACTACAGGGTCTGAC-----TCCTGGGGCCAGGGAGTCTCTGGTCACCGTCTCCCTCA	411
Db	355	actactatgacttacttcttacttggtggtccagggaaccctggtcacctgtctctca	411
RESULT 14			
AAAF69242	AAAF69242 standard; DNA; 411 BP.		
XX	AAAF69242;		
XX	17-APR-2001 (first entry)		
XX			
DE	Human antibody H chain protein SEQ ID NO:58.		
XX			
KW	Human; mouse; drug-resistant hyperglycaemia; PTHrP; cardiovascular;		
KW	parathyroid hormone related peptide; gastrointestinal; cancer;		
KW	central nervous system; calcium-antagonist; bone resorption inhibitor		
KW	bisphosphonate; calcitonin; calcium elimination promoter;		
KW	intestinal calcium absorption inhibitor; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200102012-A1.		
XX			
PD	11-JAN-2001.		
XX			
XX	06-JUL-2000; 2000WO-JP04523.		
XX			
PR	06-JUL-1999; 99JP-0192270.		
XX			
PA	(CHUS) CHUGAI SEIYAKU KK.		
XX			
PI	Saito H, Tsunenari T, Onuma E;		
XX			
DR	WPI; 2001-123066/13.		
XX			
PT	Agents inhibiting binding of parathyroid hormone related peptide to i		
PT	receptor for treatment of drug-resistant hyperglycemia -		
XX			
PS	Example; Page 95-96; 118pp; Japanese.		
XX			
CC	The present invention describes an agent (I) for the treatment of		
CC	drug-resistant hyperglycaemia. (I) contains as an active component a		
CC	substance which inhibits the binding of parathyroid hormone related		
CC	peptide (PTHrP) to its receptor. (I) is a calcium-antagonist. (I) can		
CC	be used for treatment of drug-resistant hyperglycaemia e.g. associated		
CC	with cancer. The hyperglycaemia is resistant to treatment with other		
CC	drugs including bone resorption inhibitors (such as bisphosphonate or		
CC	calcitonin), calcium elimination promoters and intestinal calcium		
CC	absorption inhibitors. AAF69197 to AAF69252 and AAB76917 to AAB76935		
CC	represent sequences used in the exemplification of the present		
CC	invention.		
XX			
SQ	Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;		

Db	121	tgtcagcctctg-----gattcaacctcagtagctatggaatgtcttgggtccgcag	174
Qy	181	GCCTCCAGGGCAGGGCGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGTATCCACACATGG	240
Db	175	gtccaggcaaggcgtgagtggtggtggaaccattagtagtggtggtgttacacctac	234
Qy	241	TACGCAGACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGACGCCAACACACACTG	300
Db	235	tatccagacagtgtgaagggtgattccattccattctccagagacaattccaagaacacgctg	294
Qy	301	TTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG	360
Db	295	tattcgaatgatcaagcgtcgagagctgagagctgaggacagcgctgtgtattactgtcgaagacag	354
Qy	361	ACTACAGGGTCTGAC-----TCCTGGGGCCAGGAGTCTCGTCCAGCGTCTCCTCA	411
Db	355	actactatgacttacttcttacttgcttacttggtggccagggaaccctggtcacgctctctca	411
RESULT	15		
AAS	22625		
ID	AAS22625	standard; cdNA; 1458 BP.	
XX			
AC	AAS22625;		
XX			
DT	24-OCT-2001	(first entry)	
XX			
DE	Human cDNA encoding a novel human protein #191.		
XX			
KW	Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;		
KW	immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;		
KW	anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;		
KW	antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;		
KW	thrombolytic; immunogen; antibody; gene therapy; neurological disorder;		
KW	Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;		
KW	tissue regeneration; immune disorder.		
OS	Homo sapiens.		
XX			
PN	W0200155437-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	25-JAN-2001; 2001WO-US02623.		
XX			
PR	25-JAN-2000; 2000US-0491404.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YT, Liu C, Drmanac RT;		
XX			
DR	WPI: 2001-451939/48.		
DR	P-PSDB; AAU14320.		
XX			
PT	Isolated polypeptides useful for treating anti-inflammatory diseases,		
PT	nervous system disorders, and for regenerating bone and cartilage -		
XX			
PS	Claim 1; Page 432-434; 894pp; English.		
XX			
CC	The invention relates to polynucleotides encoding novel human		
CC	proteins or their active domains. The polypeptides, polynucleotides and		
CC	antibodies raised against the polypeptides are used in a method of		
CC	treatment of a mammal and prevention of disorders caused by the aberrant		
CC	protein expression or activity. The polypeptides can be used as		
CC	molecular weight markers, food supplements, and in antibody production.		
CC	The polypeptides are used to identify compounds which bind to the		
CC	polypeptides. Polynucleotides of the invention are used as probes and		
CC	primers, for sequencing, for chromosome or gene mapping, in the		
CC	production of recombinant proteins, and in generating anti-sense DNA or		
CC	RNA and in gene therapy. Polypeptides of the invention can be used to		
CC	target drugs to a tumour. In assays to determine biological activity, to		
CC	raise antibodies/ elicit an immune response, to determine quantitative		
CC	protein levels, as tissue markers and to isolate receptors or ligands.		

CC Polypeptides of the invention may also be useful in treating platelet
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia, as a
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence encodes a protein of the invention.
XX

SQ Sequence 1458 BP; 353 A; 369 C; 368 G; 364 T; 4 other;

Query Match 64.7%; Score 266; DB 22; Length 1458;
Best Local Similarity 83.8%; Pred. No. 1.7e-65;
Matches 315; Conservative 0; Mismatches 55; Indels 6; Gaps 1;
QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTGTGTCCTTTTGAAGGTGCCAGTGTGAG 60
Db ||||||| ||||||| || |||| || ||||| ||||||| |||||
146 atggagtttgggctgagctgggcttttctgtgctgttttaaaagggtgccagtgtgag 205
QY 61 GTCCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTCTGG 120
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
206 gtccagctgttgagctgtgggagggctgtgtacagcctggggggtccctgagactctcc 265
QY 121 TGCGCAGCCTCCGGGTTCAGGTTTCACCTTCAATAACTACTGAGCTGGGTCCGCCAG 180
Db || ||||| || ||||| || ||||| || ||||| ||||| ||||| |||||
266 tggcagcctctg-----gattcaccttagcagctatgcatgagctgggtccgcccag 319
QY 181 GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTATCCCATGG 240
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
320 gctccaggaaagggtgagtggtctcagctattagtggtgagtggtgtagcacatac 379
QY 241 TACGCAGACTCCCTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
380 tacgcagactccctgaagggtccaggttcacatctccagagacaattcccaagaacacgtg 439
QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGCTGTCTATTACTGTGCGAGCTTG 360
Db || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
440 tatctgcaaatgaacagcctgagagccgagagacacggttatattactgtgcgaaatcc 499
QY 361 ACTACAGGGTCTGACT 376
Db || ||||| |||||
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	411	100.0	411	14	US-09-019-441-4
2	407.8	99.2	411	16	US-09-292-053-7
3	358.4	87.2	19040	17	US-09-343-485A-3
4	282.6	68.8	1710	23	US-09-617-746A-100
5	282.6	68.8	1710	24	US-09-631-451A-100
6	282.6	68.8	1721	23	US-09-617-746A-97
7	282.6	68.8	1721	24	US-09-631-451A-97
8	276.8	67.3	1709	17	US-09-359-922-264
9	276.8	67.3	1709	17	US-09-359-922-264
10	274	66.7	591	25	US-09-652-127-9891
11	274	66.7	591	27	US-09-698-010-15656
12	274	66.7	591	28	US-09-710-281-5766
13	267.4	65.1	411	16	US-09-269-332-58
14	267.4	65.1	411	18	US-09-423-800-58
15	267.4	65.1	411	37	US-10-019-501-58
16	267.4	65.1	411	37	US-10-019-571-58
17	267.4	65.1	411	37	US-10-019-785-58
18	266	64.7	1458	23	US-09-617-746A-193
19	266	64.7	1458	24	US-09-631-451A-193
20	265.8	64.7	3041	25	US-09-652-125A-9393
21	265.8	64.7	3041	25	US-09-652-127-9452
22	265.8	64.7	3041	25	US-09-652-916-10122
23	265.8	64.7	3041	27	US-09-699-999-7481
24	265.8	64.7	3041	28	US-09-710-281-5795
25	265.8	64.7	3041	28	US-09-716-475-7305
26	265.8	64.7	3041	29	US-09-726-175-3019
27	265.8	64.7	3041	29	US-09-726-176-1849
28	265.8	64.7	3041	29	US-09-726-211-1347
29	265.2	64.5	645	1	PCT-US01-08655-72
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					Sequence 7, Appli
					Sequence 3, Appli
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					Sequence 9891, Ap
					Sequence 15656, A
					Sequence 5766, Ap
					Sequence 58, Appl
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					Sequence 193, App
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					Sequence 9393, Ap
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					Sequence 10122, A
					Sequence 7481, Ap
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					Sequence 7305, Ap
					Sequence 3019, Ap
					Sequence 1849, Ap
					Sequence 1347, Ap
					Sequence 72, Appl
					Sequence 73, Appl

32 263.6 64.1 432 18 US-09-431-517-21418 Sequence 21418, A
c 33 262.2 63.8 1983 18 US-09-491-404-2415 Sequence 2415, Ap
c 34 262.2 63.8 1983 34 US-09-922-279-2415 Sequence 2415, Ap
c 35 262.2 63.8 1983 34 US-09-922-279A-2415 Sequence 2415, Ap
36 262 63.7 520 32 US-09-844-684-10 Sequence 10, Appl
37 261.6 63.6 413 16 US-09-293-972-4372 Sequence 4372, Ap
38 261.6 63.6 413 34 US-09-904-939-4372 Sequence 4372, Ap
39 261.6 63.6 1741 23 US-09-617-746A-98 Sequence 98, Appl
40 261.6 63.6 1741 24 US-09-631-451A-98 Sequence 98, Appl
41 261.2 63.6 414 8 US-08-471-986-9 Sequence 9, Appl
42 261.2 63.6 1366 18 US-09-491-404-3094 Sequence 3094, Ap
43 261.2 63.6 1366 34 US-09-922-279-3094 Sequence 3094, Ap
44 261.2 63.6 1366 34 US-09-922-279A-3094 Sequence 3094, Ap
45 261 63.5 630 32 US-09-844-684-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-019-441-4
; Sequence 4, Application US/09019441
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS

NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..411

FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..411
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-019-441-4

Query Match 100.0%; Score 411; DB 14; Length 411;

Best Local Similarity 100.0%; Pred. No. 2e-103;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGTCACGTGTGAG 60
QY 61 GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCTGGGGGTCCTTGAGACTCTGG 120
Db 61 GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCTGGGGGTCCTTGAGACTCTGG 120
QY 121 TGGCAGCTTCCGGGTTTCAGGTTTCACTTCAATAACTACTACATGGACTGGTCCGCGAG 180
Db 121 TGGCAGCTTCCGGGTTTCAGGTTTCACTTCAATAACTACTACATGGACTGGTCCGCGAG 180
QY 181 GCTCCAGGGCAGGGCTGGAGTGGTCTACGTATTAGTAGTAGTGGTATCCACATGG 240
Db 181 GCTCCAGGGCAGGGCTGGAGTGGTCTACGTATTAGTAGTAGTGGTATCCACATGG 240
QY 241 TACGCAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 241 TACGCAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACGCCAACACACTG 300
QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGGAGCTTG 360
Db 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGGAGCTTG 360
QY 361 ACTACAGGGTCTCAGTCCCTGGGGCCAGGGAGTCTCTGGTACCGCTCTCCTCA 411
Db 361 ACTACAGGGTCTCAGTCCCTGGGGCCAGGGAGTCTCTGGTACCGCTCTCCTCA 411

RESULT 2

US-09-292-053-7
; Sequence 7, Application US/09292053
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: NAKAMURA, TAKEHIKO
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
; THEREOF AS THERAPEUTICS
; FILE REFERENCE: 23522.0699
; CURRENT APPLICATION NUMBER: US/09/292,053
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 08/803,085
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
; NAME/KEY: CDS
; LOCATION: (1)..(411)
US-09-292-053-7

Query Match 99.2%; Score 407.8; DB 16; Length 411;
Best Local Similarity 99.5%; Pred. No. 1.6e-102;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 atggagtttgggctgagctggggtttctctgttctcttttgaagggtgtccagtgtag 60
QY 61 GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCTGGGGGTCCTTGAGACTCTGG 120
Db 61 gtgcagctggtggagcttggggggccttggcaaggcctgggggtcccttgagactctcc 120

Qy	121	TGCCAGAGCCTCGGGTTCAGGTTACCTTCAATACTACTAGTGGGTCCGCCAG	180
Db	121	tgcagagcctccgggttcaggttcaccttcaataactactacatgagctggtccgccag	180
Qy	181	GCTCAGGCGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCACATGG	240
Db	181	gctcagggcagggctgagtggtgtccagctattagtagtagtgatcccatg	240
Qy	241	TACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAAAGCCAAACACACTG	300
Db	241	tacgagactccgtgaaggagattcaccatctccagagagaagcccaacacactg	300
Qy	301	TTTCTTCAATGAACAGAGCTGAGAGCTGAGGACGCGTGTCTATTACTGTGGAGCTTG	360
Db	301	tttctcaaatgaacagcctgagagctgagagacgctgtctattactgtcgagcttg	360
Qy	361	ACTACAGGCTGTACTCTCTGGGGCCAGGAGTCTTGTCACCGTCTCTCTCA	411
Db	361	actacaggtgtactctctctggggccaggaggtcctggtcacgctctctcca	411
RESULT 3			
US-09-343-485A-3			
; Sequence 3, Application US/09343485A			
; GENERAL INFORMATION:			
; APPLICANT: REFF, MITCHELL R.			
; APPLICANT: BARNETT, RICHARD S.			
; APPLICANT: MCLACHLAN, KAREN R.			
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN			
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND			
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME			
; FILE REFERENCE: 037003-0275807			
; CURRENT APPLICATION NUMBER: US/09/343,485A			
; CURRENT FILING DATE: 1999-06-30			
; PRIOR APPLICATION NUMBER: 09/023,715			
; PRIOR FILING DATE: 1998-02-13			
; PRIOR APPLICATION NUMBER: 08/819,866			
; PRIOR FILING DATE: 1997-03-14			
; NUMBER OF SEQ ID NOS: 3			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 3			
; LENGTH: 19040			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA			
; OTHER INFORMATION: referred to as "Mandy"			
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Best Local Similarity 93.4%; P: 2.2e-88;			
Matches 385; Conservative 0; Mismatches 26; Indels 1; Gaps 1			
Qy	1	ATGAGATTGGGCTGAGCTGGGTTTTCTGTCTCTTTTCAAGGTCCTCAGTGTGAG	60
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Qy	61	GTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGCCAAAGCCTGGGGGGTCCCTGAGACTCTGG	120
Db	9496	gtgcagctggTggagctcTggggcgccgttgccaaagcctgggggtccctgagactctcc	9555
Qy	121	TGCCAGAGCTCCGGTTCAGGTTACCTTCAATACTACTAGTGGGTCCGCCAG	180
Db	9556	tgcagagctccgggttcaggttcaaccttcaataactactacatgagctggtccgccag	9615
Qy	181	GCTCAGGCGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCACATGG	240
Db	9616	gctccagggcaggggtgagtggggtctcaagctattagtagtagTggTgattcccatggtg	9675
Qy	241	TACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAAAGCCAAACACACTG	300

Db	9676	tacgcagactccgtgaaggscagatccaccatctccagagagacgccaagacacactg	9735
Qy	301	TTTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACAGCCTGTCTATTACTGTGCGAGCTTG	360
Db	9736	ttttctcaaatgaacagcctgagagctgagacacggtctctattactgtgcagacttg	9795
Qy	361	ACTACAGGGTCTGACT~CCTGGGGCCAGGAGTCTCTGTGCACCGTCTCCTCA	411
Db	9796	actacagggctgactccctggggcaggaggctcctggctcaacgctcctca	9847
RESULT 4			
US-09-617-746A-100			
; Sequence 100, Application US/09617746A			
; GENERAL INFORMATION:			
; APPLICANT: Tang, Y. Tom			
; APPLICANT: Liu, Chenghua			
; APPLICANT: Zhou, Ping			
; APPLICANT: Qian, Xiaohong B.			
; APPLICANT: Wang, Zhiwei			
; APPLICANT: Chen, Rui-hong			
; APPLICANT: Asundi, Vinod			
; APPLICANT: Cao, Yicheng			
; APPLICANT: Tillinghast, John			
; APPLICANT: Drmanac, Radoje T.			
; TITLE OF INVENTION: Novel Nucleic Acids and			
; TITLE OF INVENTION: Polypeptides			
; FILE REFERENCE: 21272-017CIP2A (785CIP2A)			
; CURRENT APPLICATION NUMBER: US/09/617,746A			
; CURRENT FILING DATE: 2000-07-01			
; PRIOR APPLICATION NUMBER: 09/491,404			
; PRIOR FILING DATE: 2000-01-25			
; NUMBER OF SEQ ID NOS: 220			
; SOFTWARE: pt_FL_genes Version 1.0			
; SEQ ID NO 100			
; LENGTH: 1710			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (162)..(1253)			
US-09-617-746A-100			
Query Match 68.8%; Score 282.6; DB 23; Length 1710;			
Best Local Similarity 82.8%; Pred. No. 1.3e-67;			
Matches 337; Conservative 0; Mismatches 64; Indels 6; Gaps			
Qy	1	ATGAGATTGGCTGAGCTGGGTTTCTTCTGTCTCTTTTGAAGGTTGTCAGTGTGAG	60
Db	162	atgagattggctgagctggcttttctgtgtattttaaaggtgtccagttgtgag	221
Qy	61	GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCGG	120
Db	222	gtgcagctgtgtgagctgggggagctgtgtacagcctgggggtccctgagactctcc	281
Qy	121	TGCGCAGCCTCCGGGTTTCAGCTTTCACCTTCAATAACTACTACATGACTTGGCTCGCCGAG	180
Db	282	tgtcagcctctg-----gattcacctttagcagtttttcgatgagctgggtccgcag	335
Qy	181	GCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTATCCCAACATGG	240
Db	336	gctccagggaagggttgagtggtgtctcatctattagtggttcgggttaccacatac	395
Qy	241	TACGCAGACTCCGTGAAGGCGCATTTACCATCTCCAGAGAGAACGCCAACACACATG	300
Db	396	tacgcagactccgtgaagggccggtttaccatctccagagacaaattccaagaacacgctg	455
Qy	301	TTTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACAGCCTGTCTATTACTGTGCGAGCTTG	360
Db	456	tattctgcaaatgaacagcctgagagccgagacacggtctattactgtgcgaaacgg	515
Qy	361	ACTACAGGGTCTGACTCCTGGGGCCAGGAGTCTCTGGTCCACCGTCTC	407

Db 516 ttcccgatatttgactactggtggccagggaacccctggtccacgctctc 562

RESULT 5

US-09-631-451A-100
; Sequence 100, Application US/09631451A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Chen, Rui-hong
; APPLICANT: Asundi, Vinod
; APPLICANT: Cao, Yicheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 785CIP2B
; CURRENT APPLICATION NUMBER: US/09/631,451A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 100
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(1253)
US-09-631-451A-100

Query Match 68.8%; Score 282.6; DB 24; Length 1710;
Best Local Similarity 82.8%; Pred. No. 1.3e-67;
Matches 337; Conservative 0; Mismatches 64; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
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Db 162 agggagtttgggctgagctggcttttctgtggtctattttaaagggtccagtgtag 221
|||
QY 61 GTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTGG 120
|||
Db 222 gtgcagctgtgagctgtgggagggcttggtagagcctgggggtccctgagactctcc 281
|||
QY 121 TCGGAGCCTCCGGGTTCAGGTTCACCTTCAATACTACTACATGAGACTGGTCCGCCAG 180
|||
Db 282 tgtgcagctctg-----gattcaccttttagcagtttttcgagctgggtccgcca 335
|||
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGATCCACATGG 240
|||
Db 336 gctccagggaagggtgagctgggtctctatctattagttggttcgggtaccacatac 395
|||
QY 241 TACGCAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACGCCAACACACTG 300
|||
Db 396 taagcagactcctgtaaggccggttccacctccacagagacaattcccaagaacgcgtg 455
|||
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
|||
Db 456 tatctgcaaatgaacagcctgagagccgaggaacggttcattactgtgcaaacccg 515
|||
QY 361 ACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCCACCGTCTC 407
|||
Db 516 ttcccgatatttgactactggtggccagggaacccctggtccacgctctc 562

RESULT 6

US-09-617-746A-97

; Sequence 97, Application US/09617746A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Chen, Rui-hong
; APPLICANT: Asundi, Vinod
; APPLICANT: Cao, Yicheng
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 21272-017CIP2A (785CIP2A)
; CURRENT APPLICATION NUMBER: US/09/617,746A
; CURRENT FILING DATE: 2000-07-01
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 97
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(1085)
US-09-617-746A-97

Query Match 68.8%; Score 282.6; DB 23; Length 1721;
Best Local Similarity 82.8%; Pred. No. 1.3e-67;
Matches 337; Conservative 0; Mismatches 64; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
|||
Db 162 atggagtttgggctgagctggcttttctgtggtctattttaaagggtccagtgtag 221
|||
QY 61 GTGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTGG 120
|||
Db 222 gtgcagctgtgagctgtgggagggcttggtagagcctgggggtccctgagactctcc 281
|||
QY 121 TCGGAGCCTCCGGGTTCAGGTTCACCTTCAATACTACTACATGAGACTGGTCCGCCAG 180
|||
Db 282 tgtgcagctctg-----gattcaccttttagcagtttttcgagctgggtccgcca 335
|||
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGATCCACATGG 240
|||
Db 336 gctccagggaagggtgagctgggtctctatctattagttggttcgggtaccacatac 395
|||
QY 241 TACGCAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACGCCAACACACTG 300
|||
Db 396 taagcagactcctgtaaggccggttccacctccacagagacaattcccaagaacgcgtg 455
|||
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
|||
Db 456 tatctgcaaatgaacagcctgagagccgaggaacggttcattactgtgcaaacccg 515
|||
QY 361 ACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCCACCGTCTC 407
|||
Db 516 ttcccgatatttgactactggtggccagggaacccctggtccacgctctc 562

RESULT 7

US-09-631-451A-97
; Sequence 97, Application US/09631451A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei

; APPLICANT: Chen, Rui-hong
; APPLICANT: Asundi, Vinod
; APPLICANT: Cao, Yicheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 785CIP2B
; CURRENT APPLICATION NUMBER: US/09/631,451A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 97
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (162)..(1085)
; US-09-631-451A-97

Query Match 68.8%; Score 282.6; DB 24; Length 1721;
Best Local Similarity 82.8%; Pred. No. 1.3e-67;
Matches 337; Conservative 0; Mismatches 64; Indels 6; Gaps 1;
QY 1 ATGGAGTTGGGCTGAGCTGGGCTTTCCCTTTCCCTTTTGAAGGCTCCAGTGTGAG 60
Db 162 atggaattgggctgagctggctttctctgttcttgaaggtgtccagtgtag 221
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTCTGG 120
Db 222 gtgcagctgttgagctgggagagctgtgacagcctgggggtccctgagactctcc 281
QY 121 TGGCAGCCTCGGGTTCAGGTTCACTTCAATTAAGTCTGAGCTGGGTCGCCAG 180
Db 282 tggcagcctcg-----gattcaccctttagcagttttctcagatgagctgggtccgcag 335
QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCACATGG 240
Db 336 gtcacaggagggctggagtggtctcatctattagtgtagtggtggtaccacatag 395
QY 241 TAGCGAGACTCCGTGAAGGGCAGATTTCACATCTCCAGAGAGAACGCCAACACACTG 300
Db 396 tagcgagactccgtgaagggtccaccatctccagagacaattcccaagaacacgtg 455
QY 301 TTCTTCAATGAACAGCCTGAGCTGAGGAGGAGCTCTTATTTACTGTGGGAGCTTG 360
Db 456 tatctgcaaatgaacagcctgagagccgagagacggcgctattactgtgcgaacacg 515
QY 361 ACTACAGGCTCTGACTCTCTGGGGCCAGGAGCTCTGCTGCTCACCGTCTC 407
Db 516 ttctcgtatttgactactggtgggagggaggaacccctggtcaccgtcttc 562

RESULT 8
US-09-922-264/c
; Sequence 264, Application US/09359922
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359,922
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/205,155
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264

; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-359-922-264

Query Match 67.3%; Score 276.8; DB 17; Length 1709;
Best Local Similarity 82.1%; Pred. No. 5.3e-66;
Matches 353; Conservative 0; Mismatches 52; Indels 25; Gaps 2;
QY 1 ATGGAGTTGGGCTGAGCTGGGCTTTCCCTTTCCCTTTTGAAGGCTGCCAGTGTGAG 60
Db 1546 ATGGAGTTGGGCTGAGCTGGGCTTTCCCTTTTCCCTTTTGTAGAAAGTGTCCAGTGTGAG 1487
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTCTGG 120
Db 1486 GTGCAGCTGGTGGAGTCTGGGGGAGCTTGGTCCAGCCCTGGGGGGTCCCTGAGACTCTCC 1427
QY 121 TGGCAGCCTCGGGTTCAGGTTCACTTCAATAACTACTACATGAGCTGGGTCCGCCAG 180
Db 1426 TGTGCAGCCTCTG-----GATTCACTTCAATGATTATGCCATGAGCTGGGTCCGCCAG 1373
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCACATGG 240
Db 1372 GCTCCAGGCAAGGGCTGGAGTGGGTCTCATACATTAGTAGTAGGCGGTGAGCACATAC 1313
QY 241 TAGCGAGACTCCGTGAAGGGCAGATTTCACATCTCCAGAGAGAACGCCAACACACTG 300
Db 1312 TAGCGAGACTCTGTGAAGGGCGGATTTCACCATCTCCAGAGAGAACGCCAACACTCACTG 1253
QY 301 TTCTTCAATGAACAGCCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
Db 1252 TATCTCAATGAACAGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1193
QY 361 ACTACAGG-----TCTGACTCTCTGGGGCCAGGAGCTCTTATTTACTGTGGGAGCTTG 401
Db 1192 CCCTCAGGCTGCTGTCGCTCCCTTCCACATGACTCTCTGGGGCCAGGAGGAGGAGGAGG 1133
QY 402 CGTCTCCTCA 411
Db 1132 CGTCTCCTCA 1123

RESULT 9
US-09-359-922-264/c
; Sequence 264, Application US/09359922A
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/359,922A
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/205,155
; EARLIER FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: US 09/034,341
; EARLIER FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-359-922-264

Query Match 67.3%; Score 276.8; DB 17; Length 1709;
Best Local Similarity 82.1%; Pred. No. 5.3e-66;
Matches 353; Conservative 0; Mismatches 52; Indels 25; Gaps 2;
QY 1 ATGGAGTTGGGCTGAGCTGGGCTTTCCCTTTCCCTTTTGAAGGCTGCCAGTGTGAG 60
Db 1546 ATGGAGTTGGGCTGAGCTGGGCTTTCCCTTTTCCCTTTTGTAGAAAGTGTCCAGTGTGAG 1487

Db 1546 ATGCAGTTTGGGCTGAGCTGGTTTCTTGTGCTATTTTGAAGGTGTCAGTGTGAG 1487
QY 61 GTCAGCTGTGAGTCTGGGGCGGCTTGGCAAGCTGGGGGGTCCCTGAGACTCTGG 120
Db 1486 GTCAGCTGTGAGTCTGGGGAGGCTTGGTCCAGCTGGGGGGTCCCTGAGACTCTCC 1427
QY 121 TGGCGAGCTCCGGGTTACAGTTTCACCTTCAATAACTACTACATGCACTGGGTCCGCCAG 180
Db 1426 TGTGACCTCTG-----GATTACCTTCAATGATATGCCATGAGCTGGGTCCGCCAG 1373
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTTAGTAGTGTGATCCACATGG 240
Db 1372 GCTCCAGGCAAGGGCTGGAGTGGGTCTCATACTAGTAGTGGGTGTTGACCATAC 1313
QY 241 TAGCAGACTCCGTGAAGGCGAGATTCACCATCTCAGAGAGAACCCCAACACACTG 300
Db 1312 TAGCAGACTCTGTGAAGGCGGATTCACCATCTCAGAGAGAACCCCAAGAACTCACTG 1253
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 1252 TATCTGCAATGAACAGCTGAGAGCGGAGGACACGGCTGTGTATTACTGTGCGAGAGGA 1193
QY 361 ACTACAGG-----TCTGACTCCTGGGCGGAGGAGTCTGTGCTAC 401
Db 1192 CCTCAGCGCTGCTGCTGCTCCCTCCACATGACTCCTGGGCGGAGGAACCTGTGCTAC 1133
QY 402 GCTCTCTCTCA 411
Db 1132 GCTCTCTCTCA 1123

RESULT 10
US-09-652-127-9891
; Sequence 9891, Application US/09652127
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1183-001
; CURRENT APPLICATION NUMBER: US/09/652,127
; PRIOR FILING DATE: 2000-08-30
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10475
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9891
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-127-9891

Query Match 66.7%; Score 274; DB 25; Length 591;
Best Local Similarity 82.1%; Pred. No. 2.4e-65;
Matches 345; Conservative 0; Mismatches 60; Indels 15; Gaps 2;
QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
Db 96 atggaactggggctcgcgtgggtttcttctgttctattttagaaggtgtccagtgtag 155
QY 61 GTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120
Db 156 gtgcagctgtagtctgctgggaggtttggtacagctcggggtccctcgagactctcc 215
QY 121 TGGCAGCCTCCGGTTACAGTTTCAATAACTACTACATGAGTGGGTCCGCCAG 180
Db 216 tgtgagcctctg-----gattccctttagttagtgaatgaattgggtccgccag 269
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTTAGTAGTGGGTATCCCATGG 240
Db 270 gctccaggaaggctggagtggtttctacattagtagtggtagaaccatttc 329
QY 241 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
Db 96 atggaactggggctcgcgtgggtttcttctgttctattttagaaggtgtccagtgtag 155
QY 61 GTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120
Db 156 gtgcagctgtagtctgctgggaggtttggtacagctcggggtccctcgagactctcc 215
QY 121 TGGCAGCCTCCGGTTACAGTTTCAATAACTACTACATGAGTGGGTCCGCCAG 180
Db 216 tgtgagcctctg-----gattccctttagttagtgaatgaattgggtccgccag 269
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTTAGTAGTGGGTATCCCATGG 240
Db 270 gctccaggaaggctggagtggtttctacattagtagtggtagaaccatttc 329
QY 241 TAGCAGACTCCGTGAAGGCGGAGATTCACCATCTCCAGAGAGAACCCCAACACACTG 300

Db 330 tacgcagactctgtgaaggccgattccaccattctccagagacaccccaagaactcactg 389
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 390 tatctgcaaatgaacagcctgagagccgagacacagcgtgtttattactgtcgagactc 449
QY 361 ACTACAGG-----TCTGACTCCTGGGGCGGAGTCTGTGTCACCGTCTCTCA 411
Db 450 aatagtgaggagactctttttgactactggggccagggaacccctggtcaccgctctctca 509
RESULT 11
US-09-698-010-15656
; Sequence 15656, Application US/09698010
; GENERAL INFORMATION:
; APPLICANT: Williamson, Mark
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2029-001
; CURRENT APPLICATION NUMBER: US/09/698,010
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 15684
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15656
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-698-010-15656

Query Match 66.7%; Score 274; DB 27; Length 591;
Best Local Similarity 82.1%; Pred. No. 2.4e-65;
Matches 345; Conservative 0; Mismatches 60; Indels 15; Gaps 2;
QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCTTGTCTCTTTTAAAGGTGTCAGTGTGAG 60
Db 96 atggaactggggctcgcgtgggtttcttctgttctattttagaaggtgtccagtgtag 155
QY 61 GTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120
Db 156 gtgcagctgtagtctgctgggaggtttggtacagctcggggtccctcgagactctcc 215
QY 121 TGGCAGCCTCCGGTTACAGTTTCAATAACTACTACATGAGTGGGTCCGCCAG 180
Db 216 tgtgagcctctg-----gattccctttagttagtgaatgaattgggtccgccag 269
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTTAGTAGTGGGTATCCCATGG 240
Db 270 gctccaggaaggctggagtggtttctacattagtagtggtagaaccatttc 329
QY 241 TAGCAGACTCCGTGAAGGCGGAGATTCACCATCTCCAGAGAGAACCCCAACACACTG 300
Db 330 tacgcagactctgtgaaggccgattccaccattctccagagacaccccaagaactcactg 389
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 390 tatctgcaaatgaacagcctgagagccgagacacagcgtgtttattactgtcgagactc 449
QY 361 ACTACAGG-----TCTGACTCCTGGGGCGGAGTCTGTGTCACCGTCTCTCA 411
Db 450 aatagtgaggagactctttttgactactggggccagggaacccctggtcaccgctctctca 509

RESULT 12
US-09-710-281-5766
; Sequence 5766, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.

APPLICANT: Stbdal, Hilde
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.2036-001
CURRENT APPLICATION NUMBER: US/09/710,281
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,254
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 5803
SOFTWARE: FastSeq for Windows. Version 4.0
SEQ ID NO 5766
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
US-09-710-281-5766

Query Match 66.7%; Score 274; DB 28; Length 591;
Best Local Similarity 82.1%; Pred. No. 2.4e-65;
Matches 345; Conservative 0; Mismatches 60; Indels 15; Gaps 2;
QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAGGTGTCACAGTGTGAG 60
DB 96 atggaactgggctcgctgggttttcttctgttctatttttagaaggtgtccagtgtag 155
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120
DB 156 gtgcagctggtgagctggtgggaggtttgttacagcctggagggtccctgagactctcc 215
QY 121 TGGCAGCTCGCGGTTACAGTTTACCTTCAATAACTACTACATGAGTGGTCCGCCAG 180
DB 216 tgtgtagcctctg-----gattcacctttagttagtataagaaatggtggccgcag 269
QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGTATCCCATGG 240
DB 270 gctccagggaagggtcgagtgagtggtttcatatcattagtagttagtagaaccatttc 329
QY 241 TAGCGAGACTCGGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
DB 330 tacgcagactctgtgagggccgagttccaccatctccagagacaacgccagaactcactg 389
QY 301 TTCTTCAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTCTATTACTGTGCGAGCTTG 360
DB 390 tatctgcaaatgaacagcctgagagccgagagacagcgtgtttattactgtgcgagactc 449
QY 361 ACTACAGG-----TCGACTCTCGGGCCAGGAGTCTGTCTACCGTCTCCTCA 411
DB 450 aatagtgaggagctactttttgactactggtggccagggaacctgtcaccgtctctca 509

RESULT 13
US-09-269-332-58
Sequence 58, Application US/09269332
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: WAKAHARA, YUJI
APPLICANT: YABUTA, NAOHITO
TITLE OF INVENTION: ANTIBODY AGAINST HUMAN PARATHORMONE RELATED PEPTIDES
FILE REFERENCE: 04853-0033
CURRENT APPLICATION NUMBER: US/09/269,332
CURRENT FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: PCT/JP97/03382
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: JP 255196/1996
PRIOR FILING DATE: 1996-09-26
PRIOR APPLICATION NUMBER: JP 214168/1997
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 411
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(411)
NAME/KEY: sig_peptide
LOCATION: (1)..(57)
NAME/KEY: mat_peptide
LOCATION: (58)..(411)
US-09-269-332-58

Query Match 65.1%; Score 267.4; DB 16; Length 411;
Best Local Similarity 81.3%; Pred. No. 1.5e-63;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;
QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAGGTGTCACAGTGTGAG 60
DB 1 atgggggttgggctgagctgggttttctcctgttgccttttaagaggtgtccagtgtag 60
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120
DB 61 gtgcagctggtgagctggtgggagcgtggtccagcctgggaggtccctgagactctcc 120
QY 121 TGGCAGCTCGCGGTTACAGTTTACCTTCAATAACTACTACATGAGTGGTCCGCCAG 180
DB 121 tgtgtagcctctg-----gattcacctttagttagtataagaaatggtggccgcag 174
QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGTATCCCATGG 240
DB 175 gctccagggaagggtcgagtgagtggtggcaaccattagtagttagttagttacactac 234
QY 241 TAGCGAGACTCGGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300
DB 235 tatccagacagtgtagggggcgagttccaccatctccagagacaatcccaagaacagctg 294
QY 301 TTCTTCAATGAACAGCTGAGAGCTGAGAGACAGCGCTGTCTATTACTGTGCGAGCTTG 360
DB 295 tatctgcaaatgaacagcctgagagctgagagacagcgtgtgtattactgtgcgagacag 354
QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCCAGGAGTCTGTCTACCGTCTCCTCA 411
DB 355 actactatgacttactttgttactggtggccagggaacctgtcaccgtctctca 411

RESULT 14
US-09-423-800-58
Sequence 58, Application US/09423800
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: TSUNENARI, TOSHIKI
APPLICANT: ISHII, KIMIE
TITLE OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: PCT/JP98/02116
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: JP 125505/1997
PRIOR FILING DATE: 1997-05-15
PRIOR APPLICATION NUMBER: JP 194445/1997
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 411
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(411)
NAME/KEY: sig_peptide
LOCATION: (1)..(57)
NAME/KEY: mat_peptide
LOCATION: (58)..(411)

US-09-423-800-58

```
Query Match          65.1%; Score 267.4; DB 18; Length 411;
Best Local Similarity 81.3%; Pred. No. 1.5e-63;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTTGTTCCCTTTTGAAGGTGTCAGTGTGAG 60
Db 1 atggggtttgggctgagctgggttttctctcgttctctttaaagaggtgtccagtgctcag 60

QY 61 GTGCAGCTGTGTGAGTCTGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACCTGG 120
Db 61 gtgcagctgtgtgagctgtggggggcgtgtgtccagcctgtgggggtccccgagacctcc 120

QY 121 TGGCAGCCTCCGGGTTACGTTTCACTTCAATTAACCTACTACATGAGTGGTCCGCGCAG 180
Db 121 tggcagcctctg-----gattcaccttcagtagctatggcagctgtgtgggtccgcca 174

QY 181 GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGGTATTAGTAGTAGTGTGATCCACATGG 240
Db 181 gctccagggcaggggcgtggagtgggtggcaaccattagtagtggtagttagttacacctac 234

QY 241 TAGCGACACTCCCGTGAAGGGCAGATTCCACCATCTCCAGAGAGAACGCCAACACACACTG 300
Db 241 tagcgacactcccggtgaagggcagatttcacccattctccagagacaattccagaacacgctg 294

QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 301 tttcttcaatgaacagcctgagagctgagagacacggctgtctattactgtgagagacag 354

QY 361 ACTACAGGGTCTGAC-----TCCTGGGCGCAGGGAGTCTGTGTCACCGTCTCTCTCA 411
Db 361 actacatgacttacttctgttactgtggcgagggaacctgtgtcaccgtctctctca 411
```

Search completed: September 23, 2002, 19:47:39
Job time: 7034 sec

```
RESULT 15
US-10-019-501-58
; Sequence 58, Application US/10019501
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Ameliorative agent for low vasopressin concentration
; FILE REFERENCE: PH-944-PCT
; CURRENT APPLICATION NUMBER: US/10/019,501
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: JP 11-189322
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(411)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
US-10-019-501-58
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Query Match          65.1%; Score 267.4; DB 37; Length 411;
Best Local Similarity 81.3%; Pred. No. 1.5e-63;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTTGTTCCCTTTTGAAGGTGTCAGTGTGAG 60
Db 1 atggggtttgggctgagctgggttttctctcgttctctttaaagaggtgtccagtgctcag 60

QY 61 GTGCAGCTGTGTGAGTCTGGGGGGCTTGGCAAGGCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgtgagctgtggggggcgtgtgtccagcctgtgggggtccccgagacctcc 120
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:58:52 ; Search time 662.78 Seconds
(without alignments)
1998.488 Million cell updates/sec

Title: US-09-019-441-4
Perfect score: 411
Sequence: 1 ATGAGTTTGGGTGACCTG.....TCTGTGTCACGCTCTCTCA 411

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New:
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	411	100.0	411	7	US-10-103-686-4
2	276.8	67.3	1709	5	US-09-919-002-264
3	267.4	65.1	411	6	US-10-182-018-58
4	267.4	65.1	411	6	US-10-220-149-58
5	267.4	65.1	411	7	US-10-169-003-58
6	265.2	64.5	690	7	US-10-125-237-73
7	263.4	64.1	1426	1	PCT-US02-20181-1
8	262	63.7	520	7	US-10-040-244-10
9	261	63.5	630	7	US-10-040-244-14
10	257.8	62.7	580	7	US-10-040-244-12
11	256.4	62.4	1712	6	US-10-206-008-189
12	254.6	61.9	1392	7	US-10-153-382-1
13	254.6	61.9	1392	7	US-10-153-382-4
14	254.6	61.9	1999	7	US-10-153-382-2
15	253.2	61.6	1395	7	US-10-153-382-8
16	252.6	61.5	1392	7	US-10-153-382-12
17	250.8	61.0	1605	5	US-09-629-469A-18517
18	247.6	60.2	626	5	US-09-634-754C-28
19	247.6	60.2	626	5	US-09-634-754D-28
20	247.2	60.1	407	5	US-09-918-995-16657
21	244.4	59.5	1413	7	US-10-153-382-16
22	241.8	58.8	397	7	US-10-146-502-2106
23	241.2	58.7	1792	7	US-10-158-646-54
24	240	58.4	720	5	US-09-511-939-1
25	240	58.4	720	5	US-09-968-561A-1

RESULT 1

US-10-103-686-4
; Sequence 4, Application US/10103686
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; KLOETZER, William S.
; NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; City: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10103,686
; FILING DATE: 25-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..411
; FEATURE:
; NAME/KEY: mat_peptide

ALIGNMENTS

26	239.6	58.3	496	6	US-10-206-008-401	Sequence 401, App
27	239.6	58.3	496	6	US-10-211-364-212	Sequence 212, App
28	239.6	58.3	1673	1	PCT-US02-18947-1932	Sequence 1932, Ap
29	239.6	58.3	1673	7	US-10-172-118-1932	Sequence 1932, Ap
30	238.4	58.0	348	1	PCT-US02-20332-75	Sequence 75, Appl
31	238	57.9	1664	6	US-10-206-008-198	Sequence 198, App
32	236.8	57.6	348	1	PCT-US02-20332-79	Sequence 79, Appl
33	235.4	57.3	457	6	US-10-206-008-411	Sequence 411, App
34	235.4	57.3	457	6	US-10-211-364-122	Sequence 122, App
35	235.4	57.3	457	6	US-10-222-860-318	Sequence 318, App
36	235.2	57.2	348	1	PCT-US02-20332-82	Sequence 82, Appl
37	234.4	57.0	400	5	US-09-918-995-16290	Sequence 16290, A
38	231.6	56.4	1640	6	US-10-206-008-187	Sequence 187, App
39	230.4	56.1	311	6	US-10-203-135-21308	Sequence 21308, A
40	230.4	56.1	311	6	US-10-203-135-20914	Sequence 20914, A
41	229.4	55.8	351	1	PCT-IL02-00060A-25	Sequence 25, Appl
42	229.2	55.8	1404	1	PCT-US02-11853-18	Sequence 18, Appl
43	229.2	55.8	3244	1	PCT-US02-11853-16	Sequence 16, Appl
44	228.4	55.6	4026	5	US-09-949-039-1	Sequence 1, Appl
45	226	55.0	413	5	US-09-918-995-16675	Sequence 16675, A

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; LOCATION: 58..411
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-103-686-4

Query Match 100.0%; Score 411; DB 7; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 1 ATGAGAGTTGGGCTGAGCTGGGTTTCCCTGTGTCCTCTTTGAAAGGTGTCAGTGTGAG 60
Db 1 ATGAGAGTTGGGCTGAGCTGGGTTTCCCTGTGTCCTCTTTGAAAGGTGTCAGTGTGAG 60

Oy 61 GTGCAGCTGTTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 GTGCAGCTGTTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120

Oy 121 TGGCAGGCTCCGGGTTCAAGTTCACTTCAATAACTACTACATGAGACTGGGTCCGCCAG 180
Db 121 TGGCAGGCTCCGGGTTCAAGTTCACTTCAATAACTACTACATGAGACTGGGTCCGCCAG 180

Oy 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCACATGG 240
Db 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGTATCCACATGG 240

Oy 241 TACGCAGACTCCGTGAAGGCGAGATTCAACCATCTCCAGAGAGAACGCCAACAACACACTG 300
Db 241 TACGCAGACTCCGTGAAGGCGAGATTCAACCATCTCCAGAGAGAACGCCAACAACACACTG 300

Oy 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360

Oy 361 ACTACAGGGTCTGACTCCTGGGGCCAGGAGTCTGGTCAACGTCCTCTCTCA 411
Db 361 ACTACAGGGTCTGACTCCTGGGGCCAGGAGTCTGGTCAACGTCCTCTCTCA 411

RESULT 2
US-09-919-002-264/c
; Sequence 264, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONFIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-264

Query Match 67.3%; Score 276.8; DB 5; Length 1709;
Best Local Similarity 82.1%; Pred. No. 7.6e-61;
Matches 353; Conservative 0; Mismatches 52; Indels 25; Gaps

Oy 1 ATGAGAGTTGGGCTGAGCTGGGTTTCCCTGTGTCCTCTTTTAAAGGTGTCAGTGTGAG 60
Db 1546 ATGAGAGTTGGGCTGAGCTGGGTTTCCCTGTGTCCTCTTTTAAAGGTGTCAGTGTGAG 1487

Oy 61 GTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 1486 GTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTCC 1427

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Db 235 tatccagacagtgtgaagggggtattccaccatctccagagacaattcccaagaacacgctg 294
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGCTCTATTACTGTGCGAGCTTG 360
Db 295 tatctgcaaatgaacagcctgagagctgagacacggctgtgtattactgtgcgagacag 354
QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCAGGAGTCTGTGTACCGTCTCCTCA 411
Db 355 actactatgacttacttcttactgtggccagggaacccctgtgcaccgtctctctca 411

RESULT 4

US-10-220-149-58
; Sequence 58, Application US/10220149
; GENERAL INFORMATION:
; APPLICANT: CHUGAI PHARMACEUTICAL CO., LTD.
; TITLE OF INVENTION: Tissue degradation inhibiting agent
; FILE REFERENCE: PH-1015-PCT
; CURRENT APPLICATION NUMBER: US/10/220,149
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: JP2000-52414
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(411)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
US-10-220-149-58

Query Match 65.1%; Score 267.4; DB 6; Length 411;
Best Local Similarity 81.3%; Pred. No. 1.7e-58;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAGAGTGTCACAGTGTGAG 60
Db 1 atggggtttggcgtgagctgggttttctcgtgtgctcttttaagaggtgtccagtgctag 60
QY 61 GTCAGCTGTGTGAGTCTGGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgtgagctgtggggagcgctgtccagcctgggaggtccctgagactctcc 120
QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGGACTGGTCCGCCAG 180
Db 121 tgtgcagcctctg-----gattcaacctcagtagctatggcatgtcttgggtccgcccag 174
QY 181 GCTCCAGGGCAGGGCTGGAGTGGGTCTACAGTATTAGTAGTAGTGATGCCACATGG 240
Db 175 gctccaggcaaggcgtgagtgagggtggcaaccattagtagtggtgtagttacacctac 234
QY 241 TAGCAGACTCTCCGTGAAGGCGCATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 tatccagacagtgtgaagggcgattccaccatctccagagacaattcccaagaacgctg 294
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGAGCTGAGCAGGCTGCTATTACTGTGCGAGCTTG 360
Db 295 tatctgcaaatgaacagcctgagagctgagacacggctgtgtattactgtgcgagacag 354
QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCAGGAGTCTGTGTACCGTCTCCTCA 411
Db 355 actactatgacttacttcttactgtggccagggaacccctgtgcaccgtctctctca 411

RESULT 5

US-10-169-003-58
; Sequence 58, Application US/10169003

; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical Preparation
; FILE REFERENCE: PH-1093-PCT
; CURRENT APPLICATION NUMBER: US/10/169,003
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: JP 11-375203
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(411)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
US-10-169-003-58

Query Match 65.1%; Score 267.4; DB 7; Length 411;
Best Local Similarity 81.3%; Pred. No. 1.7e-58;
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTGTTCCTCTTTTGAAGAGTGTCACAGTGTGAG 60
Db 1 atggggtttggcgtgagctgggttttctcgtgtgctcttttaagaggtgtccagtgctag 60
QY 61 GTCAGCTGTGTGAGTCTGGGGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgtgagctgtggggagcgctgtccagcctgggaggtccctgagactctcc 120
QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGGACTGGTCCGCCAG 180
Db 121 tgtgcagcctctg-----gattcaacctcagtagctatggcatgtcttgggtccgcccag 174
QY 181 GCTCCAGGGCAGGGCTGGAGTGGGTCTACAGTATTAGTAGTAGTGATGCCACATGG 240
Db 175 gctccaggcaaggcgtgagtgagggtgggtggcaaccattagtagtggtgtagttacacctac 234
QY 241 TAGCAGACTCTCCGTGAAGGCGCATTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 tatccagacagtgtgaagggcgattccaccatctccagagacaattcccaagaacgctg 294
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGAGCTGAGCAGGCTGCTATTACTGTGCGAGCTTG 360
Db 295 tatctgcaaatgaacagcctgagagctgagacacggctgtgtattactgtgcgagacag 354
QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCAGGAGTCTGTGTACCGTCTCCTCA 411
Db 355 actactatgacttacttcttactgtggccagggaacccctgtgcaccgtctctctca 411

RESULT 6

US-10-125-237-73
; Sequence 73, Application US/10125237
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chinghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhang, Jie
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and

Best Local Similarity 80.2%; Pred. No. 1.9e-57; Matches 344; Conservative 0; Mismatches 61; Indels 24; Gaps					
Qy	1	ATGAGAGTTGGGCTGAGCTGGGTTTTTCCTTGTGTCCTTTTAAAGGTGTCCAGTGCTGAG 60 	Db	14	atgagattggcgctagcgtgccttttcttgctggtcattttaaaagtgtccagtgtag 73
Qy	61	GTCGAGCTGTTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTGCCCTGAGACTCTGG 120 	Db	74	gtgcagctgttggagtcgtggagggttgtacagcgtgggggtcccctgagactctcc 133
Qy	121	TGCGCAGCCTCCGGTTTCAGGTTTCACCTTCAATAAATACATACATGAGCTGGGTCCGCCAG 180 	Db	134	tgtgcagcctctg-----gatcacacctttagcagctatgccatgagctggtgccccag 187
Qy	181	GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGATGCCACATGG 240 	Db	188	gtccagggaagggctgagtggtgtcaggtattactgtggagtggtggtagtagcatac 247
Qy	241	TACCACAGACTCCGTGAAGGCAGATTCCACCATCTCCAGAGAGAACCACCAACACACTG 300 	Db	248	tacgcagactctcg tgaaggccgggttcaccatctccagagacaaatccccagaacacgcgtg 307
Qy	301	TTTCTTCAAATGAACACCCTGAGAGCTGAGGACACAGSCTGCTATTACTGTGCGA----- 355 	Db	308	tatctgcaaatgaacacgctgagagccgagacagccgctatatattactgtgcgaaagat 367
Qy	356	-----GCTTGACTACAGGCTCTGACTCTCTGGGGCCAGGGAGTCTCTGGTCACC 402 	Db	368	ccagggaactaoggtgattagttgttcgacctgtggccacctgggcccagggaacctggtccac 427
Qy	403	GTCCTCCTCA 411 	Db	428	gtotccotca 436
RESULT 8					
US-10-040-244-10					
; Sequence 10, Application US/10040244					
; GENERAL INFORMATION:					
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA					
; APPLICANT: FORCE WALKER F.					
; APPLICANT: TAKAHASHI, NOBUAKI					
; APPLICANT: MIKAYAMA, TOSHIFUMI					
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANT					
; FILE REFERENCE: 021286/0272501					
; CURRENT APPLICATION NUMBER: US/10/040,244					
; CURRENT FILING DATE: 2002-06-17					
; PRIORITY APPLICATION NUMBER: 60/200,601					
; PRIOR FILING DATE: 2000-4-28					
; PRIOR APPLICATION NUMBER: PCT/US01/13672					
; PRIOR FILING DATE: 2001-04-27					
; PRIOR APPLICATION NUMBER: 09/844,684					
; PRIOR FILING DATE: 2001-04-27					
; NUMBER OF SEQ ID NOS: 17					
; SOFTWARE: PatentIn Ver. 3.0					
; SEQ ID NO 10					
; LENGTH: 520					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
US-10-040-244-10					
Query Match 63.7%; Score 262; DB 7; Length 520;					
Best Local Similarity 85.7%; Pred. No. 4e-57;					
Matches 305; Conservative 0; Mismatches 45; Indels 6; Gaps					
Qy	1	ATGAGAGTTGGGCTGAGCTGGGTTTTTCCTTGTGTCCTTTTAAAGGTGTCCAGTGCTGAG 60 	Db	32	atggagtttggtgagctgggttttccctgtgtcattttaaaaggtgtccagtgtag 91
Qy	61	GTCGAGCTGTTGGAGTCTGGGGCGGCTTGGCAAAAGCCTGGGGGTGCCCTGAGACTCTGG 120 			

Db	92	gtcagctggtgagagtcgcggggaagccttagttcagcctgggggggtcccttgagactctcc	151
Qy	121	TGCGCAGCCTCCGGGTTCAGGTTTCACCTTCAATAACTACTACATGACTGGTGCCGAC	180
Db	152	tgtcagtcctg-----gattcaaccttcagtaacctacttgatgacatgggtccgcca	205
Qy	181	GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTGTATCCACATGG	240
Db	206	gtccaggggaagggcgtggtggtggtctcagttatcaatgtagtggagtagcacaacc	265
Qy	241	TACGCAGACTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACACTG	300
Db	266	tacgcgactccgtgaagggccgattcaccatctccagagacaacgccagaacacgctg	325
Qy	301	TTTCTTCAATGAACGCCCTGAGAGCTGAGGACACGGCTCTCTATTACTGTGGCAG	356
Db	326	tatctgaatgaacagctctgagagcgagagcacgctgtgattactctgcaag	381

RESULT 9
 US-10-040-244-14
 ; Sequence 14, Application US/10040244
 ; GENERAL INFORMATION:
 ; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
 ; APPLICANT: FORCE, WALKER F.
 ; APPLICANT: TAKAHASHI, NOBUAKI
 ; APPLICANT: MIKAYAMA, TOSHIFUMI
 ; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBODIES
 ; FILE REFERENCE: 021286/0272501
 ; CURRENT APPLICATION NUMBER: US/10/040,244
 ; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: 60/200,601
 ; PRIOR FILING DATE: 2000-4-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/13672
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: 09/844,684
 ; PRIOR FILING DATE: 2001-04-27
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 3.0
 ; SEQ ID NO 14
 ; LENGTH: 630
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-040-244-14

[illegible]

RESULT 10
US-10-040-244-12
; Sequence 12, Application US/10040244
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIKAYAMA, TOSHIFUMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-4-28
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 12
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-12

Query Match	62.7%	Score 257.8;	DB 7;	Length 580;
Best Local Similarity	85.1%;	Pred. No. 4.7e-56;		
Matches 302; Conservative	0;	Mismatches 47;	Indels	6; Gaps
QY	1	ATGGAGTTGGGGCTGAGCTGGGTTTCTCTGTTCCTCTTTGAAAGGTGTCAGTGTGAG	60	
Db	32	atggagtttggtgctggctggtctttctctgtggtcattcttaaaaggtgccagtgtag	91	
QY	61	GTGCAGCTGTGGAGCTGTGGGGCGGCTTGGCAAGCGCTGGGGGGTCCCTGAGACTCTGG	120	
Db	92	gtcagctgttgagctcgtgggagagctgtgtacagcctggggggtccctgagactctcc	151	
QY	121	TGGCAGCCTCCGGTTCAGGTTCACTTCACTTCAATAACTACATGAGCTGGTGGCCGAG	180	
Db	152	tgtgcagctctg-----gattcgcctttagcagctatgccatgagctggtgtccgcca	205	
QY	181	GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGGTGATCCACATGG	240	
Db	206	gcctcagggaagggtctggagttgggtctcagctatgtagtggtagtggtagcacatc	265	
QY	241	TAGCGACTCTCGTGAAGGCGATTTCACCATCTCCAGAGAGAACGCCAACACACACTG	300	
Db	266	tacgcagactccgtgaaggcccggttcacccaatccagagacaattccaagaacacgctg	325	
QY	301	TTTCTTCAATGAAACGCTGTGAGCTGAGGACACGGCTCTCTATTACTGTGGCA	355	
Db	326	tactgcaaatgaacacgtctgagcgagagacacgcgcgtatctactgtcgga	380	

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RESULT 11
US-10-206-008-189
; Sequence 189, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253CIN
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/479,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04

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; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
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; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
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; PRIOR FILING DATE: 2000-09-29
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; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
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; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
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; PRIOR APPLICATION NUMBER: 60/237,038
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; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17

;; PRIOR APPLICATION NUMBER: 60/249,264
;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-11-17
;; PRIOR APPLICATION NUMBER: 60/249,297
;; PRIOR FILING DATE: 2000-11-17
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;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/231,242
;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/232,080
;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/231,244
;; PRIOR FILING DATE: 2000-09-08
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;; PRIOR FILING DATE: 2000-09-14
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;; PRIOR FILING DATE: 2000-09-14
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;; PRIOR FILING DATE: 2000-09-14
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;; PRIOR FILING DATE: 2000-09-14
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;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
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;; PRIOR FILING DATE: 2000-10-20
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;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,065

Query Match 62.4%; Score 256.4; DB 6; Length 1712;
Best Local Similarity 79.0%; Pred. No. 1.2e-55;
Matches 343; Conservative 0; Mismatches 61; Indels 30; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTGAAGGTTGCCAGTGTGAG 60
Db 66 atggagtttgggctgagctgggttttcccttgttctgttttaaaagggtgccagtgtag 125

QY 61 GTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCTGGGGGTCCTGAGACTCTGG 120
Db 126 gtgcagctggtgagtcgggggagagcttagttcagcctgggggtccctgagactctcc 185

QY 121 TGGCAGCCTCCGGGTTCAAGGTTCACTTCAATACTACATGACTGGGTCGCCAG 180
Db 186 tgtgagcgcgtg-----aattcgcttcaagtaactagtgatgcactgggtcccgccaa 239

QY 181 GTCCAGGCGAGGGGTGGAGTGGGTCTCAGCTATTAGTAGTGTGATCCCATG 240
Db 240 gtccaggaagggtgctgtatgggtcacatcttaagtgtatggaagtccacaagg 299

QY 241 TAGCAGACTCCGTGAAGGCGAGTTTCACTTCCAGAGAGAACGCCAACACACTG 300
Db 300 tagcgaactccgtgaaggccgattccatttccagagacacgtcaagaacacactt 359

QY 301 TTCTTCAATGAACGCTGAGAGTGGAGCAGCGCTGTCTATTACTGTGCGA----- 355
Db 360 tatctgcaaatgagcagtcgtgagagtcgagagcacagcgtctattacgtgtagagga 419

QY 356 -----GCTTACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCTCTG 396
Db 420 gtaaaagactggcagtagtgggttagccctgactttgactactggtggccagggaacccctg 479

QY 397 GTACCGGTCTCTCTC 410
Db 480 gtacccgtctctc 493

RESULT 12
US-10-153-382-1
; Sequence 1, Application US/10153382
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-1

Query Match 61.9%; Score 254.6; DB 7; Length 1392;
Best Local Similarity 79.4%; Pred. No. 3.3e-55;
Matches 331; Conservative 0; Mismatches 74; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTGAAGGTTGCCAGTGTGAG 60
Db 1 atggagtttgggctgagctgggttttcccttctttaaagaggtgtccagtgtag 60

QY 61 GTGCAGCTGGTGGAGTCTGGGGGCGCTTGGCAAGCCTGGGGGTCCTGAGACTCTGG 120
Db 61 gtgcagctggtgagctgggggagcggtgccagccgggaggtccctgagactctcc 120

QY 121 TGGCAGCCTCCGGGTTTCAAGGTTCACTTCAATACTACATGACTGGGTCGCCAG 180
Db 121 tgtgtagcgtctg-----gattcaccttcagtagccatggcagctgggtccgcccag 174

QY 181 GTCCAGGCGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGTGATCCCATG 240
Db 175 gtccagggcagaaggctgagtggtggtgaggttatgtatgtaggaagaaataaac 234

QY 241 TAGCAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACGCCAACACACTG 300
Db 235 tatgcagactccgtggaaggccgattccaccatctccagagacaattccaagaacgcgtg 294

QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGAGTGGAGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 295 ttctgcaaatgaacagcctgagagcggagacacggctgtgtattactgtgtagagga 354

QY 361 ACT-----ACAGGGTCTGACTCTCTGGGGCAGGAGTCTGTGTCACCGTCTCTCA 411
Db 355 ggtcactcggctctttgactactggggccagggaacccctgggtcaccgtctctctca 411

RESULT 13
US-10-153-382-4
; Sequence 4, Application US/10153382
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

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Db      121  tgtgtagcgtctg-----gattcaccccttcagtagccatggcgaactgggtccgcgcag 174
Qy      181  GCTCAGGCGCAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTGATCCACATGG 240
      |||||  |||||  |||||  |||||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      175  gctccaggccaaggcgctggagtggggtggcagttatatggtatgatggagaataaatac 234
Qy      241  TACGCAGACTCCGTGAAGGCGAGATTCAACCATCTCCAGAGAGAACGCCAACACACACTG 300
      ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      235  tatcagactccgtggaaggccgattaccatctccagagacaaattcccaagaacacgctg 294
Qy      301  TTCTTCTCAATGTAACGCCCTGAGAGCTGAGGACAGCGCTGCTCTATTACTGTGCGAGCTTG 360
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      295  ttctgcgaatgaacacgctcgagacgagacgagcagcgctgtgtattactgtgcgagagga 354
Qy      361  ACT-----ACAGGGTCTGACTCTCTGGGGCGAGGAGTCTCGTGTACACCGTCTCCTCA 411
      ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      355  ggtaacttcggtcccttttgactactggggccagggaacccctggtcaacctctctca 411

RESULT 15
US-10-153-382-8
; Sequence 8, Application US/10153382
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-8

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Query Match	61.6%	Score	253.2;	DB	7;	Length	1395;
Best Local Similarity	79.0%	Pred. No.	7.6e-55;				
Matches	332;	Conservative	0;	Mismatches	73;	Indels	15;
							Gaps
QY	1	ATGGAGTTGGCGCTGAGCTGGGTTTCCTCTGTTCCCTTTGTAAGAGGTGCCAGTGTGAG	60				
Db	1	atggagtttggcgtgagctgggttttccctcgttgcctctttaaagaggtgtccagtgccag	60				
QY	61	GTGCAGCTGTGTGGAGTCTGGGGCGGCTGGCCAAAGCCTGGGGGGTCCCTGAGACACTGG	120				
Db	61	gtcagctgtgtgagctgtgggagggcgtgttcacgacctgggaggtccctgagactctcc	120				
QY	121	TGCGCAGCCTCCGGGTTTCAGGTTCACTTCAATAACTACTACATGAGCTGGGGTCCGCCAG	180				
Db	121	tgtacagcgtctg-----gattcaccttcagtaactatggcactgactgggtccgccaag	174				
QY	181	GCTCCAGGCGAGGGCTGGAGTGGGTCTCACTGATTAGTAGTAGTGGTGATCCACATGG	240				
Db	175	gtcccaaggcaaggggcgtggagtggggttatataggatgagtaataaacac	234				
QY	241	TACGCAGACTCCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACACTG	300				
Db	235	tatggagactccgtgaaggcgagattcaccatctccagtgacaattccaagaacacgcctg	294				
QY	301	TTTCTTCAATGAACACGCTTGAGAGCTGAGGACACGGCTGCTATTACTGTGTGC-----	353				
Db	295	tatctgcaaatgaacacctgagccgagacacggctgtgtattactgtgcgagaggga	354				
QY	354	--GAGCTTTGACTACAGGGTCTGACTCTCTGGGGCCAGGGAGTCTCGTGCACCGTCTCCTCA	414				
Db	355	gagagactgggggtctactttgactactggggccagggaacacctgggtccaccgtctctctca	414				

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; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-4

Query Match          61.9%; Score 254.6; DB 7; Length 1392;
Best Local Similarity 79.4%; Pred. No. 3.3e-55;
Matches 331; Conservative 0; Mismatches 74; Indels 12; Gaps 2;

QY 1 ATGGAGGTTGGCGTGAGCTGGCGTTTCTCTGCTTCTCTTTTGAAGGNGTCCAGTGTGAG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 atggagtttgggcgagctgggtttctctgcttctctctttaaagggtggtccagtgtaac 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GTGCAGCTGTGTGAGTCTGGGGGGCGTTGGCAAGCCTGGGGGTCTCCTGAGACTCTGG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 gtgcagctgtgtgagttctgggggagcggtgttcagcctgggaggtccctgagactctcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 TGGCGACGCTCCGGGTTTCAGGTTCCACTTCAATTAACACTACTACATGGAGTGGTCCGCCAG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 tgttagcgctcg-----gattcaccttcagtagcattggcatgcactgggtccgcgacg 174
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 GCTCCAGGGCAGGGCGTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCCACTATGG 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 gctccaggcaagggtcgagtggtggagtttatatgtgatgtgagaagaataaataac 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 241 TACGCACACTCCGTGAAGGGCAGATTACCACTATCCAGAGAGAGCGCCAAACAACACTG 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 235 tatgcagactcgttgaagggtccgattcaccaatctccagagagacaattccaagaaacacgctg 294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTCCGAGCTTG 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 295 ttctgcaaatgaacgccitgagagcgagacacgctgtgttattactgtgcagagaga 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 361 ACT-----ACAGGGTGTGACTCTCTGGGGCAGGGATGCTGTGTCACCGTCTCTCTCA 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 ggtcactctcgctcttttgtagtactgtgggcagaggaacacctggtcacccgtctctcca 411
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RESULT      14
US-10-153-382-2
; Sequence 2, Application US/10153382
; GENERAL INFORMATION:
; APPLICANT: PEIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: FC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; PRIORITY FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-2

Query Match          61.9%; Score 254.6; DB 7; Length 1999;
Best Local Similarity 79.4%; Pred. No. 3.4e-55;
Matches 331; Conservative 0; Mismatches 74; Indels 12; Gaps 2;

QY    1   ATGCAGTTTGGCTGACGTGGGTTTTCTTGTTCTCTTTTGAAGGTGCCAGTGTGCG 60
Db     1   atggagtttggctgagctgggtttcttcgtctcttttaaggagtgtccagtgtcag 60
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
QY    61   GTGCAGCTGTGGAGTCTGGGGGGGGCTTGCAAGCCTGGGGGTCCCTGAGACTCTGG 120
Db     61   gtgcagctgttgagttctggggggggcggtgccagcctgggaggtccctgagactctcc 120
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
QY    121  GTGGCAGCCTCCGGGTTTCAGGTTCACCTTCAATAACTACTACTATGTGAGTGGTCCGCCAG 180
Db     121  gtggcagcctccggggttcaggttcaccttcaataactactactatgtgagtggtccgccag 180
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

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Search completed: September 23, 2002, 19:58:58
Job time: 7188 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 18:00:53 ; Search time 110.65 Seconds
(Without alignments)
912.385 Million cell updates/sec

Title: US-09-019-441-4
Perfect score: 411
Sequence: 1 ATGGAGTTTGGGTGACGTG.....TCCTGGTCACCGTCTCTCA 411

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	411	100.0	411	3	US-08-803-085-4
2	259.8	63.2	432	1	US-08-026-320A-1
3	252.2	61.4	393	1	US-08-259-372A-3
4	252.2	61.4	393	1	US-08-468-671-3
5	241.8	58.8	423	1	US-08-259-372A-1
6	241.8	58.8	423	1	US-08-468-671-1
7	236.2	57.5	519	3	US-08-545-809A-21
8	236.2	57.5	743	3	US-08-545-809A-48
9	235.6	57.3	715	3	US-08-545-809A-11
10	231.8	56.4	417	4	US-08-134-346A-49
11	227.6	55.4	514	3	US-08-545-809A-23
12	225.8	54.9	405	4	US-08-619-491-7
13	225.8	54.9	405	5	PCT-US95-07302-7
14	225.2	54.8	426	1	US-08-305-683A-1
15	224.2	54.5	1572	3	US-09-049-672A-18
16	223.4	54.4	649	3	US-08-545-809A-64
17	222.4	54.1	413	1	US-08-253-877C-56
18	222.4	54.1	413	2	US-08-452-164A-56
19	222	54.0	418	1	US-07-977-696C-27
20	222	54.0	418	1	US-08-129-930B-27
21	222	54.0	418	4	US-08-976-288A-27
22	221.4	53.9	543	4	US-08-862-124-1
23	221.4	53.9	543	4	US-08-862-124-3
24	220.8	53.7	908	4	US-09-273-839A-9
25	220.6	53.7	354	2	US-08-652-816A-21
26	220	53.5	354	2	US-08-652-816A-22
27	219.2	53.3	348	2	US-08-652-816A-24

28	218.8	53.2	474	2	US-08-653-402B-5	Sequence 5, Appli
29	218.6	53.2	724	3	US-08-545-809A-53	Sequence 53, Appl
30	217.2	52.8	423	2	US-08-646-367-1	Sequence 1, Appli
31	217	52.8	514	3	US-08-545-809A-20	Sequence 20, Appl
32	216.4	52.7	445	1	US-08-053-171-10	Sequence 10, Appl
33	216.4	52.7	491	1	US-08-053-171-6	Sequence 6, Appli
34	216.2	52.6	405	4	US-08-619-491-3	Sequence 3, Appli
35	216.2	52.6	405	5	PCT-US95-07302-3	Sequence 3, Appli
36	216	52.6	405	4	US-08-579-378A-19	Sequence 19, Appl
37	215.6	52.5	892	4	US-09-273-839A-11	Sequence 11, Appl
38	214.4	52.2	640	3	US-08-545-809A-9	Sequence 9, Appli
39	214.2	52.1	1576	1	US-08-157-101A-6	Sequence 6, Appli
40	213.8	52.0	512	3	US-08-545-809A-30	Sequence 30, Appl
41	212.4	51.7	474	2	US-08-653-402B-9	Sequence 9, Appli
42	212.2	51.6	351	2	US-08-428-197-35	Sequence 35, Appl
43	212.2	51.6	351	5	PCT-US93-10555-35	Sequence 35, Appl
44	211.8	51.5	424	2	US-08-765-783A-62	Sequence 62, Appl
45	211.8	51.5	424	3	US-08-921-100-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-803-085-4
; Sequence 4, Application US/08803085
; Patent No. 601138
; GENERAL INFORMATION:
; APPLICANT: REFF, Mitchell E.
; APPLICANT: KLOETZER, William S.
; APPLICANT: NAKAMURA, Takehiko
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,085
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..411
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..411
US-08-803-085-4

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Query Match      100.0%; Score 411; DB 3; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.6e-112;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GTCCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAAGCTTGGGGGTCCTGAGACTCTCG 120
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QY 181 GTCCAGGCGAGGGGCTGGAGTGGGTCCTCAGCTATTAGTAGTGGTATCCCATCG 240
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QY 361 ACTACAGGCTGTGACPTCTGGGGCCAGGAGTCCGTGCTCAGCTCTCCCTCA 411
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RESULT 2

US-08-026-320A-1
; Sequence 1, Application US/08026320A
; Patent No. 5419904

; GENERAL INFORMATION:
; APPLICANT: Irie, Reiko F
; TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
; TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Poms, Smith, Lande & Rose
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States of America
; ZIP: 90067

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,320A
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/609803
; FILING DATE: 05-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J
; REGISTRATION NUMBER: 29421
; REFERENCE/DOCKET NUMBER: 94268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310785046
; TELEFAX: 3102771297
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; CELL TYPE: Epstein Barr Virus Transformed B cell  
; CELL LINE: L612  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..432  
; OTHER INFORMATION: /function= "Heavy Chain"  
; OTHER INFORMATION: /product= "Immunoglobulin Variable Region"  
; OTHER INFORMATION: /standard_name= "Humab L612 Heavy Chain Variable  
; OTHER INFORMATION: Region Sequence"  
; FEATURE:  
; NAME/KEY: misc_feature  
; LOCATION: 148..162  
; OTHER INFORMATION: /function= "Complementary  
; OTHER INFORMATION: determining region 1 (CDR1)"  
; FEATURE:  
; NAME/KEY: misc_feature  
; LOCATION: 271..300  
; OTHER INFORMATION: /function= "Complementary  
; OTHER INFORMATION: determining region 2 (CDR2)"  
; FEATURE:  
; NAME/KEY: misc_feature  
; LOCATION: 397..429  
; OTHER INFORMATION: /function= "Complementary determining  
; OTHER INFORMATION: region 3 (CDR3)"  
; US-08-026-320A-1
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Query Match 63.2%; Score 259.8; DB 1; Length 432;

Best Local Similarity 79.9%; Pred. No. 1.5e-67;

Matches 338; Conservative 0; Mismatches 67; Indels 18; Gaps 2;

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Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTTCCCTTTTGAAGGTCTCCAGTGTGAG 60
    |||||||

QY 61 GTCCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAAGCTTGGGGGTCCTGAGACTCTCG 120
    |||||||
Db 61 GTCCAGCTGGTGGAGTCTGGGGGGGCTTGGTACAGCTTGGGGGTCCTGAGACTCTCC 120
    |||||||

QY 121 TGGCAGCTCCGGGTTGAGTTTCCCTCAATACTACTACATGAGTGGTCCGCCAG 180
    |||||||
Db 121 TGTGAGCTCTG-----GATTCACCTTTAGCAGCTGTGCCATGAGCTGGGTCCGCCAG 174
    |||||||

QY 181 GTCCAGGCGAGGGGCTGGAGTGGGTCCTCAGCTATTAGTAGTGGTATCCCATGG 240
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Db 175 GTCCAGGCGAAGGGGCTGGAGTGGGTCCTCAGCTATTAGTGGTGGTGGTAGCATAC 234
    |||||||

QY 241 TAGCCAGACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAACGCCAACACACTG 300
    |||||||
Db 235 TAGCCAGACTCCGTGAAGGCGGCTTCCATCTCCAGAGAACATCCCAAGACAGTTG 294
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QY 356 -----GCTTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCTGTGTCACCGTCTCC 408
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Db 355 GGCAACAGATATTTTGACTGGTTATTATGCTTGGGGCCAGGAAACCTGTGTCACCGTCTCC 414
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QY 409 TCA 411
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Db 415 TCA 417
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RESULT 3

US-08-259-372A-3
; Sequence 3, Application US/08259372A

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Patent No. 5565354
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: ZM1-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..393
US-08-259-372A-3

Query Match 61.4%; Score 252.2; DB 1; Length 393;
Best Local Similarity 81.5%; Pred. No. 2.6e-65;
Matches 335; Conservative 0; Mismatches 58; Indels 18; Gaps 3;

QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTTCCCTTTTGAAGAGGTGCCAGTGTGAG 60
DB 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTTCCCTTTTGAAGAGGTGCCAGTGTGAG 60

Patent No. 5565354
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: ZM1-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..393
US-08-259-372A-3

QY 61 GTGCAGCTGGTGGAGTCTGGGGGCGGCTTTGGCAAAAGCCTGGGGGGTCCCTGAGACTCTCG 120
DB 61 GTGCAGCTGGTGGAGTCTGGGGGCGGCTTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCG 120
QY 121 TCGGCAGCCTCCGGGTTGAGTTCACCTTCAATAACTACTACATGAGCTGGGTCCGCCAG 180
DB 121 TGTGACGCTCTG-----GATTCACCTTCAGTAGTAGACATGTACTGGGTCCGCCAA 174
QY 181 GCTCCAGGCGAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGGTATCCACATGG 240
DB 175 GCTACAGGAAAGGCTGCGAGTGGGTCTCAGCTATTGGTCTCTACTGTGA---CACATAC 231
QY 241 TAGGCAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACCCCAACACACTG 300
DB 232 TATGCAGACTCCGTGAAGGCGGATTTCACCATCTCCAGAGAGAAATCCCAAGAACTCCTTG 291
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DB 292 TATCTTACAATGAACGCTGAGAGCGGCGGACACGCGGTGTGTATTACTGTGGAAG---- 347
QY 361 ACTACAGGCTCTGACTCTCTGGGCGGAGGAGTCTGCTGACCGCTCTCTCA 411
DB 348 -----AGATTTAGAACTCTGGGCGGAGGAAACCTGTGTCACCGTCTCTCA 393

RESULT 4
US-08-468-671-3
Sequence 3, Application US/08468671
Patent No. 5648077
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
```

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: ZM1-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..393
US-08-468-671-3

Query Match 61.4%; Score 252.2; DB 1; Length 393;
Best Local Similarity 81.5%; Pred. No. 2.6e-65;

Matches 335; Conservative 0; Mismatches 58; Indels 18; Gaps 3;

QY 1 ATGGAGCTTTGGGCTGAGCTGGGTTTCCCTGTCTCTTTTGAAGGTGCCAGTGTGAG 60
DB 1 ATGGAGCTTTGGGCTGAGCTGGGTTTCCCTGTCTCTTTTGAAGGTGCCAGTGTGAG 60
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DB 232 TATGACAGCTCCGTGAAGGCGGATTACCATCTCCAGAGAGAAATGCCAAGAACTCTTG 291
QY 301 TTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTGTCTATTACTGTGGAGCTTG 360
DB 292 TATCTTACAATGAACGCTGAGAGCGGGGACAGCGCTGTGTATTACTGTGCAAG---- 347
QY 361 ACTACAGGCTGACTCTCTGGGCGGAGGAGTCTGGTCAACGCTCTCTCA 411
DB 348 -----AGATTGAACTCTGGGCGGAGGAGACCCCTGGTCAACGCTCTCTCA 393

RESULT 5

US-08-259-372A-1

Sequence 1, Application US/08259372A

Patent No. 5565354

GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.

TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: PE1-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..423
US-08-259-372A-1

Query Match 58.8%; Score 241.8; DB 1; Length 423;

Best Local Similarity 82.3%; Pred. No. 3e-62;

Matches 292; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

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QY 181 GCTCCAGGCGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATGCCATCCACATGG 240
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Db 235 TAGCAGACTCGTGAAGGCGAGATTACCATCTCCAGAGAGAACCCCAACACACTG 294
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Db 295 TTTCGCAATGCACAGCTGAGAGCTGCGGACACGGGTGTATATTACTGTGCGA 349

RESULT 6

US-08-468-671-1
; Sequence 1, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,671
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,372
; FILING DATE: 14-JUN-1994
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: Hybridoma

; CELL LINE: PE1-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..423
US-08-468-671-1

Query Match 58.8%; Score 241.8; DB 1; Length 423;

Best Local Similarity 82.3%; Pred. No. 3e-62;
Matches 292; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTTCCCTCTTTTGAAGGCTGTCCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTTTCCCTCTTTTGAAGGCTGTCCAGTGTGAG 60
QY 61 GTCCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTCTG 120
Db 61 GTCCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTCTG 120
QY 121 TCGGAGCCTCCGGGTTTCAGGTTTCAGCTTCAATTAATACTACTAGTGGTCCGCCAG 180
Db 121 TGTGCAGCCTCTG-----GATTCACCTTCAGTAGGTATGGCATGCACTGGGTCCGCCAG 174
QY 181 GCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTATCCCATG 240
Db 175 GCTCCAGGCGAAGGGGCTGGAGTGGGTGGCAGTATCATATGATGAAGTAATAATG 234
QY 241 TAGCAGACTCGTGAAGGCGAGATTACCATCTCCAGAGAGAACCCCAACACACTG 300
Db 235 TATGCAGACTCGTGAAGGCGGATTACCATCTCCAGAGAGAACCCCAACACACTG 294
QY 301 TTTCCTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 355
Db 295 TTTCGCAATGCACAGCTGAGAGCTGCGGACACGGGTGTATATTACTGTGCGA 349

RESULT 7

US-08-545-809A-21
; Sequence 21, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-21

Query Match 57.5%; Score 236.2; DB 3; Length 519;
Best Local Similarity 85.0%; Pred. No. 1.5e-60;
Matches 278; Conservative 0; Mismatches 43; Indels 6; Gaps 1;
QY 30 TGTTCCTCTTTTGAAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 89
DB 141 TGTCTCTCTGTTTGCAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 200
QY 90 GCAAGAGCTGGGGTCCCTCAGACTCTGCTGCGCAGCTCCGGGTTTCAGGTTCACCTT 149
DB 201 GGTCAAGCTGGGGTCCCTCAGACTCTCCTGTCGAGCTCTG-----GATTCACCTT 254
QY 150 CAATAACTACTACATGAGTGGTCCGCCAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTC 209
DB 255 CAGTAGCTATACATGAACCTGGTCCGCCAGGCTCCAGGAAGGGCTGAGTGGGTCTC 314
QY 210 AGCTATTAGTAGTGGTGATCCACATGTTACGAGACTCCGTTGAAGGGCAGATTTCAC 269
DB 315 ATCCATTAGTAGTAGTGGTGATCCACATGTTACATATACGAGACTCAGTGAAGGGCGATTTCAC 374
QY 270 CATCTCCAGAGAGAGCGCCCAACACACTGTTCTTCAAAATGAACAGCTGAGAGCTCA 329
DB 375 CATCTCCAGAGAGAGCGCCCAACACACTGTTCTTCAAAATGAACAGCTGAGAGCTCA 434
QY 330 GGACAGGCTGTCTATTACTGTGCGAG 356
DB 435 GGACAGGCTGTCTATTACTGTGCGAG 461

RESULT 8
US-08-545-809A-48
Sequence 48, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 743 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-48

Query Match 57.5%; Score 236.2; DB 3; Length 743;
Best Local Similarity 85.0%; Pred. No. 1.7e-60;
Matches 278; Conservative 0; Mismatches 43; Indels 6; Gaps 1;
QY 30 TGTTCCTCTTTTGAAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 89
DB 306 TGTCTCTCTTGTGTCAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 365
QY 90 GCAAGAGCTGGGGTCCCTCAGACTCTGCTGCGCAGCTCCGGGTTTCAGGTTCACCTT 149
DB 366 GTATAGCTGGGGTCCCTCAGACTCTCCTGTCGAGCTCTG-----GATTCACCTT 419
QY 150 CAATAACTACTACATGAGTGGTCCGCCAGGCTCCAGGCGAGGGGCTGGAGTGGGTCTC 209
DB 420 CAGTAGCTATACATGAACCTGGTCCGCCAGGCTCCAGGAAGGGCTGAGTGGGTCTC 479
QY 210 AGCTATTAGTAGTGGTGATCCACATGTTACGAGACTCCGTTGAAGGGCAGATTTCAC 269
DB 480 ATACATTAGTAGTAGTGGTGATCCATATACGAGACTCTGTGAAGGGCGATTTCAC 539
QY 270 CATCTCCAGAGAGAGCGCCCAACACACTGTTCTTCAAAATGAACAGCTGAGAGCTCA 329
DB 540 CATCTCCAGAGAGAGCGCCCAACACTGATCTGCAAAATGAACAGCTGAGAGCTCA 599
QY 330 GGACAGGCTGTCTATTACTGTGCGAG 356
DB 600 GGACAGGCTGTCTATTACTGTGCGAG 626

RESULT 9
US-08-545-809A-11
Sequence 11, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996

```

> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: PCT/JP93/00603
> FILING DATE: 10-MAY-1993
> ATTORNEY/AGENT INFORMATION:
> NAME: Freeman, John W.
> REGISTRATION NUMBER: 29,066
> REFERENCE/DOCKET NUMBER: 06501/004001
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 617-542-5070
> TELEFAX: 617-542-8906
> TELEX: 200134
> INFORMATION FOR SEQ ID NO: 11:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 715 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: double
> TOPOLOGY: linear
> MOLECULE TYPE: Genomic DNA
> ORIGINAL SOURCE:
> ORGANISM: Homo sapiens
> CELL TYPE: human lymphoblast
> CELL LINE: CGM1
> US-08-545-809A-11

```

Query Match	57.3%	Score 235.6	DB 3	Length 715
Best Local Similarity	84.8%	Pred. No. 2.5e-60		
Matches 278	Conservative 0	Mismatches 44	Indels 6	Gaps 1
Qy	29	TTGTTCCCTCTTTTGAAGGTCTCCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCT	88	
Db	331	TTGTCTCTGTGTTTGCAGGTGTCAGTGTCCAGGTGCAGCTGGTGGAGTCTGGGGAGGCT	390	
Qy	89	TGGCAAGCCCTGGGGGGTCCCTGAGACTCTCTGGTGCAGCCTCCCGGTTTCAGGTTTCACCT	148	
Db	391	TGGTCAAGCCCTGGAGGGTCCCTGAGACTCTCTCTGTGCAGCCTCTG-----GATTTCACCT	444	
Qy	149	TCAATPACTACTACATGAGACTTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCT	208	
Db	445	TCAGTGACTACTACATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGT	504	
Qy	209	CACGTATTAGTAGTAGTGGTGATCCACATGTTAGCGACAGCTCCCTGAAGGCGCAGATTCA	268	
Db	505	CATACATTTAGTAGTAGTGGTAGTACCATPATACTACGCAGACTCTCTGTGAAGGCCGAGTTCA	564	
Qy	269	CCATCTCCAGAGAACGCCCAACACACACTGTTTCTTTCATTAATGAACAGCCTGAGAGCTG	328	
Db	565	CCATCTCCAGGCAACGCCAAGAACTACACTGTATCTCTCAATGAACAGCCTGAGAGCGG	624	
Qy	329	AGGACACGGCTCTATTACTGTGGAG	356	
Db	625	AGGACACGGCGCTGTTACTGTGGGAG	652	

RESULT 10
US-08-134-346A-49
; Sequence 49, Application US/08134346A
; Patent No. 6281335

: GENERAL INFORMATION:
 : APPLICANT: do Couto, F. J. R.
 : APPLICANT: Ceriani, R. L. C.
 : APPLICANT: Petersen, J. A.
 : TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
 : TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
 : TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
 : NUMBER OF SEQUENCES: 51
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Osträger, Chong & Flaherty
 : STREET: 300 Park Avenue
 : CITY: New York
 : STATE: NY
 : COUNTRY: US
 : ZIP: 10022-7499

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-826-6365
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PS-08-134-346A-49

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Query Match	56.4%	Score	231.8	DB 4	Length	417	
Best Local Similarity	76.1%	Pred. No.	2.6e-59				
Matches	319	Conservative	0	Mismatches	82	Indels	18
Gaps							

Qy	1	ATGAGATTGGGCTGAGCTGGGTTTCCTGTGTCCTCTTTGAAAGGTGTCAGGTGTGAG	60
Db	1	ATGACATTTTGGGCTCAGCTTGGTTTCTTCTGTCCTATTATTTAAAGGTGTCAGGTGTGNA	60
Qy	61	GTGACGTGTGTGGAGTCTGTGGGGGGGCTTTGGCAAGCGTGGGGGTGCCTCGAGACTCTGG	120
Db	61	GTGCAGATGTGTGGAGTCTGTGGGGAGGCTTAGTGCAGCGCTGGAGGGTCCCTGAGACTCTCC	120
Qy	121	TGCGCAGCTCCGGGTTCAGTTCACCTTCATTAATACTACTACATGACTGGGTGCGCCAG	180
Db	121	TGTGAGGCTCTG-----GATTCGCTTCAGTACTGATGCACTGTCTTGGGTTCGCCAG	174
Qy	181	GCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGTATTAGTAGTGTGTGATCCCATCTGG	240
Db	175	GCTCCAGGAAGGGCTGGAGTGGGTGCAGAAATTAGTAGTGTGTGTAATTACGCCATC	234
Qy	241	TACGAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAAAGCCCAACAACTGTG	300
Db	235	TATCAAGACACTGTACGGGGCGATTTCACCATCTCCAGAGACAATTCCAAGAACAACCTG	294
Qy	301	TTTCTTCAAAATGAACAGCTCAGAGCTCAGACACGGCTGCTATTACTGTGCGA-----	355
Db	295	TACCTGCAAAATGAACAGTCTGAGGCTCAGGACACGGCCGTATTACTGTCCAGGGAG	354
Qy	356	-----GCTTGACTACAGGCTGTGACTCTCTGGGGCCAGGGAGTCCCTGGTCAACGTC	407
Db	355	GACTACGGTATTCGCGGCTGCTTTCCTTACTTGGGGCCAGGGAGCTGTGCTACTGTCTC	413

RESULT 11
US-08-545-809A-23
; Sequence 23, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston

QY 361 ACTACAGGCTGACTCCTGGGCGGAGTCTGGTCAACGCTCTCTCA 411
Db 355 TTACCCCGCTTGTCTACTTGGGGCCAAAGGACTTTGGTCACTGTCTCTGCA 405

RESULT 13

PCT-US95-07302-7
; Sequence 7, Application PC/TUS9507302
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,963
; FILING DATE: 14-JUNE-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-005810PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..405
PCT-US95-07302-7

Query Match 54.9%; Score 225.8; DB 5; Length 405;
Best Local Similarity 73.7%; Pred. No. 1.5e-57;
Matches 303; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

QY 1 ATGGAGCTTTGGCTGAGCTGGGTTTCCCTGCTCTCTCTTTGAAAGGTCTCCAGTGTGAG 60
Db 1 ATGGAGCTCAGGCTCAATTTAGTTTCTCTGCTCTTATTTAAAGGTCTCCAGTGTGAA 60
QY 61 GTGCAGCTGGTGGAGTCTGGGCGGCTTGGCAAGCCTGGGGGTCCCTGAGACTCTGG 120
Db 61 GTACAACTGGTGGAGTCTGGGCGGAGTTTGTGACGCTGGAGGTCCTCTCTCTCC 120
QY 121 TGGCAGCTCCGGGTTCAAGTTTCAATTAATACTACATGAGCTGGGTCCGCCAG 180
Db 121 TGTGAGCCTCTG-----GATTCTTTTCACTAGTCTTTTGAATGCACTGGGTCTGTCAG 174
QY 181 GCTCCAGGCGAGGGCTGAGTGGGTCTCAAGTATTTAGTAGTGGTATCCACATGG 240
Db 175 GCTCCTGGTAAAGGGCTGGAGTGGGTCTGCAATTCATTAGCAGTGGCAGTAGTACCATCTAC 234
QY 241 TAGCGAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300

Db 235 TATGCTGACACAGTGAAGGGCGGATTCACCATCTCCAGAGACACACAGACACCTTG 294
QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGGCTGTCTATTACTGTGCGAGCTTG 360
Db 295 TATCTGCAATGAACAGTCTAAGGGCTGAGGACACAGCGCTGTATTACTGTGCAAGACCT 354
QY 361 ACTACAGGCTGACTCCTGGGCGGAGTCTGGTCAACGCTCTCTCA 411
Db 355 TTACCCCGCTTGTCTACTTGGGGCCAAAGGACTTTGGTCACTGTCTCTGCA 405

RESULT 14

US-08-305-683A-1
; Sequence 1, Application US/08305683A
; Patent No. 5646041
; GENERAL INFORMATION:
; APPLICANT: HARFELDT, Elisabeth
; APPLICANT: LAKE, Philip
; APPLICANT: NOTTAGE, Barbara
; APPLICANT: OSTBERG, Lars G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,683A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,279
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-005230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..426
; OTHER INFORMATION: /product= "HSV863 heavy chain
; OTHER INFORMATION: variable region"
US-08-305-683A-1

Query Match 54.8%; Score 225.2; DB 1; Length 426;
Best Local Similarity 79.2%; Pred. No. 2.3e-57;
Matches 282; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTTCTCTTTTGAAGGTGTCCAGTGTGAG 60
Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTTCTCTTTTGAAGGTGTCCAGTGTGAG 60

QY 61 GTCAGCTGTGAGTCTGGGGGGGGTGGCAAGCGCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 GTCAGCTGTGAGTCTGGGGGGGGTGGCAAGCGCTGGGGGGTCCCTGAGACTCTCC 120
QY 121 TGGCAGCTCCCGGTTTCAGGTTTCACCTTCAATAACTACTACATGAGCTGGTCCGCCAG 180
Db 121 TGTGACGCTCTG-----GATTCACCTTCAGTAGCCATGTCATGATGGGTCCGCCAG 174
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCACATGG 240
Db 175 GCTCCAGGCAAGGGCTGCAGTGGCTGGCAGTTACATGGTACGATGAAGTACAAGCC 234
QY 241 TAGCGAGACTCCCTGAAGGCGAGATTCACCATCTCCAGAGAGAACGCCCAACACACTG 300
Db 235 TATGGAGAGTCCGTGAAGGCCGATTCATCATCTCCAGAGACAATTCACAAGATATCCTG 294
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACACGCTGTCTATTACTGTGCGAG 356
Db 295 TATCTGCAATGAACAGCTGAGAGCGGAGGACACGCTGTGTATTACTGTGCGAG 350

RESULT 15

US-09-049-672A-18
; Sequence 18, Application US/09049672A
; Patent No. 6135941

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/049,672A

; FILING DATE: HEREWITH

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0497 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1572 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: BMARNOT03

; CLONE: 1669829

; US-09-049-672A-18

Query Match 54.5%; Score 224.2; DB 3; Length 1572;
Best Local Similarity 79.2%; Pred. No. 7.6e-57;
Matches 281; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

QY 1 ATGAGCTTTGGGCTGAGCTGGGTTTTCCTTGTTCCCTTTTGAAGGTGTCCAGTGTGAG 60
Db 64 ATGGAGTTGGGACTGAGCTGGATTTCCTTTTGGCTATTTTAAAGGTGTCCAGTGTGAA 123
QY 61 GTCCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCGCTGGGGGGTCCCTGAGACTCTGG 120
Db 124 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAGGTCCCTGAGACTCTCC 183
QY 121 TGGCAGCTCCCGGTTTCAGGTTTCACCTTCAATAACTACTACATGAGCTGGGTCCGCCAG 180
Db 184 TGTGACGCTCTG-----GATTCACCTTTGTGATGACCATGCCATGCACTGGGTCCGCCAA 237
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTATCCCATGG 240
Db 238 ATTCCAGGGAAGGGCCTGGAGTGGGTCTCAGGTATTAAATTGGCATAGTGTACCATAGGC 297
QY 241 TAGGCAGACTCCCTGAAGGCGAGATTTCACCATCTCCAGAGAGAACGCCCAACACACTG 300
Db 298 TATGCGAAGCTCTGTAAAGGGCGGATTTCACCATCTCCAGAGACAACGCCCAAGAGCTCCCTG 357
QY 301 TTTCTTCAATGAACAGCTGAGAGCTGAGAGCGCTGAGGACACGCTGTCTATTACTGTGCGA 355
Db 358 TATCTGCAATGAACAGCTGAGAGTTGAGGACACGCTTTGATATATTGGGGCTA 412

Search completed: September 23, 2002, 18:00:56

Job time: 3227 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:50:25 ; Search time 6364.12 Seconds
(without alignments)
1325.809 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

Sequence: 1 ATGGCTGGACTGCTCCT.....CCCGTTGACCGTCCTAGGT 390

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	100.0	390	14	US-09-019-441-1
2	390	100.0	390	16	US-09-292-053-1
3	334	85.6	605	33	US-09-878-134-264
4	334	85.6	605	37	US-10-033-356-264
5	330.8	84.8	607	17	US-09-396-885-4438
6	330.8	84.8	607	17	US-09-396-885A-4438
7	328.8	84.3	419	16	US-09-287-618-20661
8	327.6	84.0	841	55	US-60-168-599-592
9	327.4	83.9	465	17	US-09-359-087-41768
10	324.4	83.2	408	16	US-09-235-076-36573
11	324.4	83.2	408	16	US-09-277-227-16098
12	324.4	83.2	408	17	US-09-332-782-36573
13	324.4	83.2	408	29	US-09-737-223-36573
14	324.4	83.2	408	34	US-09-909-627-16098
15	324.4	83.2	421	16	US-09-235-076-16692
16	324.4	83.2	421	16	US-09-289-768-1488
17	324.4	83.2	421	17	US-09-332-782-16692
18	324.4	83.2	421	29	US-09-737-223-16692
19	324.4	83.2	421	35	US-09-939-397-1488
20	324.2	83.1	509	25	US-09-652-127-62
21	322.8	82.8	430	17	US-09-359-087-5162
22	322.8	82.8	508	26	US-60-665-486-564
23	322.8	82.8	508	55	US-60-168-599-294
24	322.4	82.7	1460	1	PCT-US02-04175-8
25	322.4	82.7	1460	37	US-10-076-747-8
26	322.2	82.6	425	17	US-09-359-087-38195
27	321.2	82.4	379	18	US-09-489-036-8482
28	321.2	82.4	379	35	US-09-943-143-8482
29	321.2	82.4	862	26	US-09-665-486-563
30	321.2	82.4	862	55	US-60-168-599-293
31	321.2	82.4	891	14	US-09-049-672-23
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 264, App
					Sequence 264, App
					Sequence 4438, Ap
					Sequence 20661, A
					Sequence 592, App
					Sequence 41768, A
					Sequence 36573, A
					Sequence 16098, A
					Sequence 36573, A
					Sequence 16098, A
					Sequence 16992, A
					Sequence 16992, A
					Sequence 1488, Ap
					Sequence 62, Appli
					Sequence 5162, Ap
					Sequence 564, App
					Sequence 294, App
					Sequence 8, Appli
					Sequence 38195, A
					Sequence 8482, Ap
					Sequence 8482, Ap
					Sequence 563, App
					Sequence 293, App
					Sequence 23, Appli

QY 61 TGTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGGACAGTCGCGTACCAATCTCC 120
Db 92 tctgcccctgacctcagcgtccctccgtgtctggtctcttggagcagtcgataccactctcc 151
QY 121 TGCACCTGGAAACAGCAGTACGCTTGGTGTATTAACATATGTCTCTCTGGTACCAACACAC 180
Db 152 tgcactggaaacagcagtgacgttggtgagtagtaataactatgtctctctggtaacaaacagcac 211
QY 181 CCAGGCAAGCCCCAACTCATGATTTATGATGTCGTAAGCGGCCCTCAGGGTCTCT 240
Db 212 ccaggcaaaagccccaaactcatgattatgatgtcagtaataatcgccctcaggggtttct 271
QY 241 GATCGCTTCTCTGGCTCCCAAGTCTGCAACACGGCTCCTCCTGACCATCTCTGGGCTCCAG 300
Db 272 aatcgcttctctggctcccaagctctggcaacagcgctccctgacctatctctgggtccag 331
QY 301 GCTGAGGACGAGCTGATTATTATTACTTGTTCATATACAAACAGTACAGTACGATCTTGTATTTC 360
Db 332 gctgaggacagagcgtgattattactgacgtcatatatacaagaacactcttggtgatttc 391
QY 361 GGAAGAGGACCGGTTGACCTGCTAG 388
Db 392 ggcggagggaaccaagtgtaccgtcctag 419

RESULT 8

US-60-168-599-592
; Sequence 592, Application US/60168599
; GENERAL INFORMATION:
; APPLICANT: Hodgson, David M. Jones, Anissa L.
; APPLICANT: Lincoln, Stephen E. Yu, Jimmy Y.
; APPLICANT: Russo, Frank D. Greenawalt, Lila B.
; APPLICANT: Spiro, Peter A. Panzer, Scott R.
; APPLICANT: Banville, Steve C. Roseberry, Ann M.
; APPLICANT: Bratcher, Shawn R. Wright, Rachel J.
; APPLICANT: Cohen, Gerard E. Chen, Wensheng
; APPLICANT: Rosen, Bruce Liu, Tommy
; APPLICANT: Shah, Purvi Yap, Pierre E.
; APPLICANT: Chalup, Michael S. Anshey, Stefan
; APPLICANT: Hillman, Jennifer L. Fong, Willy Tuen
; TITLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES
; FILE REFERENCE: PT-0099 P
; CURRENT APPLICATION NUMBER: US/60/168,599
; CURRENT FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 737
; SOFTWARE: PERL Program
; SEQ ID NO 592
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 255510.168
US-60-168-599-592

Query Match 84.0%; Score 327.6; DB 55; Length 841;
Best Local Similarity 90.0%; Pred. No. 3.7e-83;
Matches 351; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGGCTGGACTCTGCTCTGCTCACTCCTCCTCACTCAGGCGCACAGGATCTCTGGGCTCAG 60
Db 34 atggcctggcctctgctctattctaccctccctcactcagggcacagggctctgggccag 93
QY 61 TGTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGGACAGTCGCGTACCAATCTCC 120
Db 94 tctgcccctgacctcagcgtccctccgtgtctggttctctgagcagtgataccactctcc 153
QY 121 TGCACCTGGAAACAGCAGTACGCTTGGTGTATTAACATATGTCTCTCTGGTACCAACACAC 180
Db 154 tgcactggaaacagcagtgacgttggtgagtagtaataactatgtctctctggtaacaaacagcac 213

QY 181 CCAGGCAAGCCCCAACTCATGATTTATGATGTCGTAAGCGGCCCTCAGGGGCTCTCT 240
Db 214 ccaggcaaaagccccaaactcatgattatgatgtcagtaataatcgccctcaggggtttca 273
QY 241 GATCGCTTCTCTGGCTCCCAAGTCTGCAACACGGCTCCTCCTGACCATCTCTGGGCTCCAG 300
Db 274 aatcgcttctctggctcccaagctctggcaacagcgctccctgacctatctctgggtccag 333
QY 301 GCTGAGGACGAGCTGATTATTATTACTTGTTCATATACAAACAGTACAGTACGATCTTGTATTTC 360
Db 334 gctgaggacagagcgtgattattactgacgtcatatatacaagaatcttactcaggggtttc 393
QY 361 GGAAGAGGACCGGTTGACCTGCTAGGT 390
Db 394 ggcggagggaaccaagtgtaccgtcctaggt 423

RESULT 9

US-09-359-067-41768
; Sequence 41768, Application US/09359067
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-747CONI
; CURRENT APPLICATION NUMBER: US/09/359,067
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: US 09/131,598
; EARLIER FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 49786
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41768
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-359-067-41768

Query Match 83.9%; Score 327.4; DB 17; Length 465;
Best Local Similarity 91.3%; Pred. No. 3.6e-83;
Matches 359; Conservative 0; Mismatches 31; Indels 3; Gaps 1;
QY 1 ATGGCTGGACTCTGCTCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCAG 60
Db 55 atggcctggcctctgctgctctcctcctcctcctcactcagggcacagggctctgggccag 114
QY 61 TGTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGGACAGTCGCGTACCAATCTCC 120
Db 115 tctgcccctgacctcagcgtccctccgtgtctggttctctctggagcagtcgataccactctcc 174
QY 121 TGCACCTGGAAACAGCAGTACGCTTGGTGTATTAACATATGTCTCTCTGGTACCAACACAC 180
Db 175 tgcactggaaacagcagtgacgttggtgagtagtaataactatgtctctctggtaacaaacagcac 234
QY 181 CCAGGCAAGCCCCAACTCATGATTTATGATGTCGTAAGCGGCCCTCAGGGGCTCTCT 240
Db 235 ccaggcaaaagccccaaactcatgattatgatgtcagtaataatcgccctcaggggtttct 294
QY 241 GATCGCTTCTCTGGGTCCCAAGTCTGCAACACGGCTCCTCCTGACCATCTCTCTGGGCTCCAG 300
Db 295 aatcgcttctctggctcccaagctctggcaacagcgctccctgacctatctctgggtccag 354
QY 301 GCTGAGGACGAGCTGATTATTATTACTTGTTCATATACAAACAGTACGACT---TTGTTTA 357
Db 355 gctgaggacagagcgtgattattactgacgtcatatatacaagaagcagcagcactcccgtgta 414
QY 358 TTCGGAAGAGGACCGGTTGACCGTCTAGGT 390
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Db 31 atggcctgggtctgtctgtctcaccctctcactcagggcacagggctcctgggccccag 90
QY 61 TGTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
Db 91 tctgcccactgactcagcctgcctccgtgtctgtgggtctcctcctggacagtcgatcaccatctcc 150
QY 121 TGCACCTGGAAACGACGATGACGTTGGTGGTTATTAACATATGTCTCTGGTACCAACCCAC 180
Db 151 tgcactggaaacacagcagtgacattggtttacaaccatgtctcctggtaaccaaacac 210
QY 181 CCAGGCAAGCCGCCAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT 240
Db 211 ccaggcaagcccccaaacctcatgattatgaggtcagtaatcggccccctcagggtttct 270
QY 241 GATCGCTTCTGTGGTCCCAAGTCTGGCAACACAGGCTCCCTGACCATCTCTGGGCTCCAG 300
Db 271 aatcgcttctgtgctccaagctcgcaacacgacctccctgacctctctgtgggtccag 330
QY 301 GCTGAGGACGAGCTGATTATTACTGTTGTTTCATATACACCAAGTAGCACTTTGTTATTC 360
Db 331 gctgaggacgaggtgattattactgagctcctacatacaagcagcgatcactctgtggtc 390
QY 361 GGAAGAGGACCCGGTTGACCGTCTAGGT 390
Db 391 ggcggagggaaccaagctgacctcctggtc 420

Search completed: September 23, 2002, 19:47:11
Job time: 7006 sec